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	1.631		242		W69301	Humanised anti-IL-8 6G	4.36e-117
``	26.24		242		W69333	humanised	
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		H-1.	218	, -	67656M	Mus musculus anti-IgE	2.530-91
•	***	ľ	7		W95664	Mus musculus anti-IqE	2.536.91
:;		A.A.	2.2		M1 4563	Humanised anti-L-selec	2.53e-91
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Anti-IL-8 humanised antibody 6G4VIIN35A.F(ab/)2.
Anti-IL-8 humanised antibody of chimeric antibody; monoclonal antibody; mouse, w Humanised antibody chimeric antibody; monoclonal antibody; mouse, w Humanised antibody; chimeric chimeric, immunocherapy; psoriasis; inflammatory bowel disease, crohn's disease; ulcerative colitis; is chemic reperfusion; adult respiratory distress syndrome; schaemic reperfusion; adult respiratory distress syndrome; is chaemic reperfusion; adult respiratory distress syndrome; remarkitis; meningitis; encephalitis; uveitis; autoimmune disease; remarkitis; meningitis; sjorgen's syndrome; vasculitis, utoimmune disease; leukocyte diapedesis, multiple organ injury syndrome; septicaemia; w trauma; alcoholic hepatitis; pneumonia; pleurisy; alveolitis; wasculitis, bronchitis, bronchiectasis; cystic fibrosis; diagnosis; chimeric - mus sp.
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the complementarity determining regions (CPPs) of murine anti-1L-8 antibody 564.2.5 (see W69309) light chain within a human 5-subgroup I light chain template. Humanised anti-1L-8 monoclonal antibodies (MADS) and variants are described for use in diagnostic applications and in the treatment of inflammatory disorders. The invention provides onjugates of an antibody fragment and a non-proteinaceous polymer, such as PEG, that have improved half-life, mean residence time, and/or clearance rate compared to non-derivatised parental antibody fragment. Also claimed are a polypeptide that is an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKKNIAFLLASMFVFSIATNAYADIQMTQSPSSLSASVGDRVTITCRSSQSLVHGIGATY 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         syndrome, vasculitis, diseases involving leukocyte diapedesis, central nervous system inflammatory disorder, multiple organ injury syndrome secondary to septicaemia or trauma, alcoholic hepatitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bacterial pneumonia, antigen-antibody complex mediated diseases, inflammations of the lung, including pleurisy, alveolitis, vasculitis, pneumonia, chrochic bronchitis, bronchiectasis, and systic fibresis. They can also be used in diagnostic applications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 1679; DB 1; Length 242; Best Local Similarity 100.0%; Pred. No. 4.36e-117; Matches 242; Conservative 0; Mismatches 0; Indels 0
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Sequence 242 AA;
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PST Example K; Fig 41B-D; 328pp; English.

This is the amino acid sequence of a polypeptide encoded by charmed and sequence of a polypeptide encoded by plasmid p6G4VIIN35A.F(ab')2 (see V44953) comprising a murine-human confinence of a polypeptide antine-human confinence of thimeric described for use in diagnostic applications and in the treatment of inflammatory disorders. The invention provides conjugates of an antibody fragment and a polymer, such as PEG, that the treatment of inflammatory disorders. The invention provides conjugates of an antibody fragment and a polymer, such as PEG, that the conjugates can be used for immune therapy of e.g. psoriasis, responses associated with inflammatory bowel disease (such as crown adults, uveltis, autoimmune therapy of e.g. psoriasis, antitis, syndrome, dermatitis, diseases involving leukocyte diapedesis, central nervous system inflammatory disorder, multiple organ inflammationes econdary to septicaemia or trauma, multiple organ inflammationes econdary to septicaemia or trauma, mediated diseases, inflammations of the lung, including pleurisy, anvented is pronchectasis, and cystic fibrosis. Arronic bronchitis, vasculitis, pneumonia, antigen-antibody complex processes in the lung, including pleurisy, bronchectasis, and cystic fibrosis.
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Humanised anti-IL-8 6G4V1N35E light chain.
Humanised anti-IL-8 6G4V1N35E light chain.
Humanised antibody: monoclonal antibody: interleukin-8;
Humanised antibody: monoclonal antibody: therapy;
G34V1N35E, inflammation, immunotherapy, therapy;
psoriasis;
inflammatory bowel disease; Crohn's disease; ulcerative colitis;
ischaemic reperfusion; adult respiratory distress syndrome;
dermatitis; meningitis; encephalitis; uveitis; autoimmune disease;
rheumatoid arthritis; Sjorgen's syndrome; vasculitis;
leukocyte diapedesis; multiple organ injury syndrome; septicaemia;
                                                                                                                                                                                                                            covalently attached
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Local Similarity 100.0%; Pred No. 4 368-117;
es 242; Conservative n. ...
                                                                                                                                                                                                                            New conjugates of antibody fragments - having
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                                             22-JAN-1998; US-012116.
21-FEB-1997; US-804444.
                                                                                                   (GETH ) GENENTECH INC.
                        20-FEB-1998; U03337
                                                                                                                                                                         98-467563/40.
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vismilits, brondalits; brondientasis; eystk, librosis, diagnosis.
Nimorio - Homo sapiens,
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/no.e= "SIII leader peptide"
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11.1.23
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LL JAN 1978, US 012720.
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Monoblonal antibody specific for interiorable ensure for treuting IL-8 mediated inflammatory diseases, e.g. ulcerative colliss Disclosure Fig 27a-B; Epp: English.
This is a chimeria Fab 514. It comptished to empirementality determining regions (TFEs) of a interior backet warfable region of the multine species and light chain constant region of the human immunoulobulin 1961. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "complementarity determining region 1; determined by Kabat sequence companison"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "complementarity determining rogion 1; determined by X-ray crystallography"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "complementarity determining region 2. determined by Kabat segience comparison"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "complementarity determining medion 2; determined by X:ray crystallography"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'complementarity determining region 3, determined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "complementatify determined region 3, determined by X-ray crystallography"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chimeric Fab is used to construct a plasmid p66425chir2 which consists if marker than war althoughts of the 19th and heavy chains of 664.25 by varieties standard recombinant themselves. The recombinant human marker than 1st has much intervenence (incomparity and can inhibit the ILP binding to human neutrophisms. This activity and can inhibit the ILP binding to human neutrophisms. This intillies to ten to zero in the treatment of intervene mediated inflammatory diseases and in the treatment of interative collisis and
                                                                  121 HVPLISGGGTKVEIKHIVAAPSVEIFPPSDEGIKSGIASVVGILNNFYFPEAKVONKVDN 180
                                 121 HVELTESÇSTRVETKETVAAFSVETFFFFFFFTASTASTASTVILLANFEFFARAVÇMEVDA 180
                                                                                                                                                                                                                                                              W33745;
01-MAY-1998 (first entry)
Chimeric antline monocional antibody (634.2.5) light thain.
murine light chain, 664-25; human interleuking: II-8: anti II-8;
monocional antibody, diagnosis, inflammatory disorder, treatment:
pneumonia, complementatity determining region. CDR, variable region:
constant region. chimeric: p66425chim2, uiverative collits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "murine light chain variable region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "human light chain constant region"
                    by Kabat sequence comparison"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-MAR-1994; US-205861.
03-MAR-1994; US-205864.
(GETH.) GENENTECH INC.
Degrechuk CM. Forg S. Hebert CA. Kim KJ. Leong SR;
WPI: 98-076425/07.
                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1. .23
/note= "signal peptide of STII"
                                                                                                                                                                                                                                                 W33745 standard; Protein; 242 AA.
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                                                                                                                                                                                                                                                                                                                                                                                       Chimeric - Mus sp.
Chimeric - Homo sapiens.
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01-MAR-1995; 398611
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                                                                                                                                         241 EC 242
                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
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Murine variable region and human constant region light chain sequence.
Light chain: heavy chain: monoclonal antibody; interleukin-8; IL-8; inflammtory disorder; bacterial pneumonia, neutrophil chemotaxis, anti IL-8 monoclonal antibody; IL-8 mediated elastase release;
Streptococcus pneumoniae. Escherichia coli, Fseudomonas acruginosa; ulcerative colitis.
                                                                                                                                                                                                                                                                                                                                                                       121 HVPLTFGGGTKVEIKRIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN 180
                                                                                                                                                                                                                                                                                                                               121 HVPLIFGAGTKLELKRAVAAPTVFIFPPSSEQLKSGTASVVCLLNNFYPPEAKVQWKVDN 180
                                                                                                                                                                                                                                                                                                                                                                                                                           181 ALQSGNSQESVIEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 ALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG 240
                                                                                                                                                                                                                                    61 LHWYLUKPSYSPKILLYKVSNRESSVPDRESGSGSGTPFTFRISFVEAEDLGLYFCSQST 120
                                                                                                                                                                                                                                                                                61 LHWYQQKPGKAPKILIYKVSNRFSGVPSRFSGSGSGIDFILIISSLQPEDFATYYCSQST 120
                                                                                                                                        1 MEENIAFILLASMEVESIATNAYADIVMTQTPLSUPVSIGDQASISCRSSQSLVHGIGNTY 60
                                                                                                                                                                                    1 MKKNIAFILASMEVESIATNAYADIQMIQSPSSLSASVGDRVTITCRSSQSLVHGIGATY 60
                                                                                           Gars
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "complementarity determining region (GDP) as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "complementarity determining region (CDR)
indicated by X-ray crystallography"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "complementarity determining region (GDE) indicated by Kabat sequence comparision"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note- "complementarity determining region (CDR)
indicated by Kabat sequence comparision"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CDR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   indicated by X-ray crystallography"
                                               Length 242;
                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114
.e= "murine variable light region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "human constant light region"
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(INDV ) UNIV INDIANA.
Dogrschuk CM, Fong S, Hebert CA, Kim KJ, Leong SR;
                                            Score 1510; DB 1; 7
Pred. No. 4.89e-104;
                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note* "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W42323 standard; Frotein; 242 AA.
W42323;
                                            0uery Match
Best Local Similarity 87.6%;
Matches 212; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .125
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  242 AA;
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01-MAR-1995:
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    Sequence
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for interleukin-8; inhibits lung inflammatory conditions
profit for interleukin-8; inhibits lung inflammatory conditions
profit for interleukin-8; inhibits lung inflammatory conditions
profit for interleukin-8; inhibits lung inflammatory conditions
contibody 664.2; light chain variable region and a human light
chain constant region The 664.2; antibody is an anti-rabbit
contibody 664.2; light chain variable region and a human light
contibody 664.2; light chain variable region and a human light
contibody 664.2; light chain variable region and a human light
contibody sorters and miletary of cells in response to inflammatory
contibody, such as adult respiratory distress syndrome
(ARDS), septic shock and multiple organ failure. Treatment of bacterial
antibody, such as, e.g. humanised 664.2; that binds human IL-8 annoclonal
antibodies are especially for treating pneumonia caused by Streptococcus
pneumoniae, E. coli or platelet factor 4. IL-8 specific monoclonal
antibodies are especially for treating pneumonia caused by Streptococcus
pneumoniae, E. coli or pseudomonas aeruginosa in humans. The antibodies
confidammatory, conditions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 ALQSGNSQESVTEQDSKDSTVSLSSTLTLSKADYEKHKVYACEVTHGGLSSPVTKSFNRG 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HVPLIFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKKNIAFLLASMFVFSIATNAYADIVWTQTPLSLPVSLGDQASISCRSSQSLVHGIGNIY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKKNIAFLLASMFVFSIATNAYADIQMTQSPSSLSASVGDPVTITCPSSQSLVHGIGATY 60
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Chimeric 664.2.5 light chain.
Monoclonal antibody 634.2.5, Mak, interleukin-8, IL-8,
chimeric antibody; Fab, antibody engineering; inflammation;
inflammatory bowel disease; ulcerative colitis; bacterial pneumonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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'note = "murine light chain variable region"
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/note= "CDR-1 location determined by Kabat
sequence comparison, amino acids 49-59
constitute CDR-1 determined by X-ray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1510; DB 1; Length 242
Pred. No. 4.89e-104;
17; Mismatches 13; Indels
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/note= "STII signal peptide"
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1. .23
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R86323 standard; Protein; 242 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 87 6%;
ses 212; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137
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Chimeric Homo sapiens.
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N-PSDB; V03226
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Disclosure, Fig 27A-Bi 63pp: English.
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Best Local Similarity 87.6%; Pred. No. 4.89e-104:
Matthes III, Conservation II, Mismarcher II (1841)
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                                                                                                                                                                                                                                                                                                                                      Treating asthma by admin, of interleukin-8 antagonist - pref. an antibody that inhibits binding of IL-8 to neutrophil(s), neutrophil chemotraxis and elastase release.

Example 4: Fig. 27: 101pp: English.

Methods for treating asthma in mammals with interleukin-8 (IL-8)
antagonists (anti-IL-8 antibodies) have been produced. Murine 664.2.5
antagonists (anti-IL-8 antibodies) have been produced. Murine 664.2.5
antagonists the murine 664.2.5 variable light chain region and the human 1961 constant light chain region chimeric monoclonal antibody. Anti-IL-8 antibodies are especially used to treat or prevent allergic asthma in humans. They inhibit: (a) neutrophil chemotaxis in response to IL-8 (b) it.8-mediated release of elastase from neutrophils and (c) binding of IL-3 to neutrophils. Anti-IL-8 antibodies can be used to treat many
                                   "MONOVING (first entry)
Chimeric monoclonal antibody light chain region.
Interleukin-8: IL-8: antagonist: anti-interleukin-8 antibody: asthma:
Inflammatory disorder; neutrophil chemotaxis; elastase release;
Inflammatory disorder; neutrophil chemotaxis; elastase release;
Inflammatory boxel disease; mouse; human.
Chimeric-Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 LHWYLAK PROSPRILLIYKVSNPPSGVPDPFSGSGSGTDFTLFISPVEAEDLGLYFGSQST 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        other inflammatory disorders, e.g. ischaemic reperfusion, ARDS, dermatitis. particularly bacterial pneumonia and inflammatory bowel
                                                                                                                                                                                                                                                                                                                                                                                                                                 /iabel= CDR_#1
/note= "According to Kabat sequence comparison"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "According to Kabat sequence comparison"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to Kabat sequence comparison"
                                                                                                                                                                                                                                                                                                                                      .abel - Murine_664.2.5_cariable_light_chain
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117. .125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "According to X-ray crystallography"
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Pred. No. 4.89e-104;
17; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note" "According to X-ray crystallography
                                                                                                                                                                                                                                                                                                                                                               138. .242
/label= Human_IgG1_constant_light_chain
                                                                                                                                                                                                                                         Location/Qualifiers
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97-118712/11
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W13790 standard, Frotein, 242 AA
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/label= CD
                                                                                                                                                                                                                                                                                                        .137
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26-JUN-1996; U11033,
27-JUN-1995; US-491334,
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                                                                                                                                                                                                                   Chimeric-Homo sapiens.
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Hebert CA, Kabakoff F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 AA;
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Imminotherapy of ulcerative colitis - with monoclonal antibody specific for interleukin-8
Example B, F4g 27; 63pp. English.
This sequence represents the light chain of a chimeric monoclonal antibody (Mab) composed of murine Mab 6G4.2.5 variable light chain and a human constant light region This Mab is used in a novel method for
                                                                                                                                                                                                                                                                                                                                                                                                                                  03-JUN-1998 (first entry)
Chimeric Mab 604.2.5 protein light chain.
Monoclonal artibody, Mab 664.2.5, interleutin-8, IL-8, murine:
ulcerative colitis; immunotherapy; bacterial pneumonia; variable region:
treatment; light chain; heavy chain; neutrophil chemotaxis inhibitor;
constant region; human.
                     61 LHWYQQKPGKAPKLLIYKVSNRFSGVPSRFSGSGSGTDF1LIISSLQPEDFATYYCSQST 120
                                                                 HVPLTFGAGTKLELKPAVAAPTVFIFPPSSEQLKSGTASVVCLLNNFYPPEAKVQWKVDN 180
                                                                                                                HVPLTFGGGTKVEIKRIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPPEAFVQWKVDN 180
                                                                                                                                                         /label= CDR_#1
/note= "alternative complementarity determining
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Fong S, Hebert CA. Kim KJ, Leong SR;
WPI: 98-100296/09.
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03-MAR-1994; US-205864;
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01-MAR-1995; 396851
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Then the inversity multis which involves the administration of an unit the accordinal antibody capable of binding to human interleuking (ii.e.) with a K4 of 19-14 to 19-11 K. This Mab also inhibits neutrophill they have taken to 19-11 K. This Mab also inhibits neutrophill they are to the binding of the transparse release by accurately and down of the bind to 5a, beta 4G or platebet factor 4. The unithodies on also be ased for the treatment of bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 LHWYLOKPOOSPYLLIYMYSNPESGVPOPFSGSGSGTDFILPISFVEAEDLGLYFOSOST 129
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Prod. No. 4.898-104;
17. Michaldhys 13, Indels O. Daps
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Anti-II-8 mouse burnen chimeric 6G4 2.5 Fab light chain.
Anti-II-8 mouse burnen chimeric anti-List. Imminotherapy, psociasis
functionatory bosed disease. Technis disease, observative collics.
Influentory bosed disease. Technis disease, syndrome disease.
Isolately in replicated to the phalitis, aveitis, autoimmine disease.
Hermanick of Hipper Collics Sjorace syndrome, vasculitis, autoimmine disease.
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/www."complementarity determining region device devermined by Mabat sequence comparison.
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determined by Kabat sequence comparison"
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                                                                                                                                                                                                                                                                                             Shorter "laman o distant light region"
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                                                                                                                                                                                                                                       138 .242
/label= Constant
                                                                                                                                    119. .124
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21-FEB-1997; US-804444.
(GEIH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                 20-FEB-1998; U03337
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New stable aqueous antibody formulations - comprising an antibody not subjected to lyephilisation, a buffer maintaining the pil at 4.5 - 6, a surfactant and a polyol bisclosure; Fig 21A: 87pp; English.

Disclosure: Fig 21A: 87pp; English.

The sequence is that of the pSil30 encoded light chain of a humanized murine anti-CDIB antibody rhumAb CDIB: It can be used for the treament of disorders which include hammorrhagic shock, thermal injury (such as that resulting from burnes), stroke (including ischeemic and hammorrhagic stroke) and myorardial infarction. The antibody formulation can be stabilised at a temperature of 2.9 deg. C for at least one year or at a temperature of 30 deg. C for at least one year or at a temperature of 30 deg. C for at least one want is stable following freezing and thawing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant humanised anti-CD18 antibody rhumab CD18 light chain.
Pecombinant humanised anti-CD18 antibody: rhumab CD18; leucine zipper;
myrine monoclonal antibody: mumab H52; protein recovery; filtration:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55 LNWYQQKPGKAPKLLIYYTSTLHSGVPSRFSGSGSGTDYTLTISSLQPEDFATYYCQQGN 115
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                                                                                                                                          pS1130 expression cassette encoded rhuMAb CD18 light chain. Macclinal activity. Neary diali. Numanized, Tycordial infarction, burns: thermal injury, ischemic, shock; ischaemic; haemorrhagic; hemorrhagic; stroke; light chain.
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W30634 standard: protein: 237 AA.
W30534:
                           W95622 standard, Protein; 237 AA. W95622.
08-JUN-1999 (first entry)
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Lam XM. Oeswell JQ. Ongpipaltan
Wang SX. Weissburg PF, Weig PL,
WPI; 99-080860,707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-JUN-1998; U12209.
13-JUN-1997: US-874897
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es 220, Conserv
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Synthetic.
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WC9856418-Al.
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Treating with reagent and filtering to remove reagent

Example; Fig 4. 43pp; English

Example
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Protein encoded by Fab-display antibody vector phMB4-19-1.6.
Murine; humanised antibody: VEGF-induced angiogenesis: tumour:
anti-vascular endothelial growth factor antibody; anti-VEGF antibody:
retinal disorder, age-related macular degeneration, diabetic retiniparing rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sample, preventing contamination. The present sequence represents the recombinant humanised anti-CD18 antibody (rhuMAb CD18) light chain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 ALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56 LNWYQQKPGKAPKLLIYYISTLHSGVPSRFSGSGSGTDYTLTISSLQPEDFATYYCQQGN 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               176 ALGSGNSGESVIEGDSKDSIYSLSSTLILSKADYEKHKVYACEVIHGGLSSPVIKSFNRG 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKKNIAFLLASMFVFSIAINAYADIQMTQSPSSLSASVGDRVTITCRASQD----INN-Y 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sits
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 TLPPIFGQGTKVEIKRIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 237;
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Sequence 237 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

Query Match

87.0%; Score 1461; DB 1; L

Bet Local Similarity 90.9%; Pred. No. 294e-100;

Matches 120; Conservative Meratches 12.
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(GETH ) GENENTECH INC.
Baca M. Chen YM. Lowman HB, Presta LG, Wells JA:
WPI; 98-568337/48.
                                                                                                                                                                                                                                                                           Blank GS, Narindray DS, Zapata GA;
WPI; 99-060267/05.
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W70703 standard; Protein; 237 AA.
W70703;
/label- signal
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03-APR-1998, HOKKO4
06-AUG-1997, US-908469.
                                                                                                                                   12.00M·1998, U12334.
13-00M-1997; US-050951.
                                                                                                                                                                                                                                       (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; X03840.
                                   W09856808-A1.
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W09845331-A2.
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241 EC 242
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237 AA:

Sequence

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Example of Fig WA-E; It pp. Enailsh.

The present sequence is exceeded by the Fab display antibody vector plant is sed in the course of the layenion. The special foliation of the special foliation of describes been inside antibodies. The humanised antibodies are endothelial arrowth factor (anti-VESF) antibodies. The humanised antibodies are used to initial Wash induced discreteris, particularly for treating any present in the present of an appropriate factor and disorders (e.g. agenolated antibodies). The present of an arrow of a disorders factor and investigation and a second conditions that involve anglogenesis, e.g. rheumatoid
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Notice vertex.
New Lumanoset and Drody with attinity for Mascalar endothelial growth
The formal sections of the Company of the formal disease and other
methorenic Stress also related moderic adid vectors and
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Light chain of 405 Fab 146 antibody - recognises HER-2 receptor
bimunised D43 antibod, hawan growth humanat, h58, selection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polonitar and outblind ration, proteins - comprises fusing ger
ear that eld, from his homour to part of M13 phage coat protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  uribilis, psoriasis, atherosimierosis, Grane's disease, etc
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Base St. Tarrand LD, Organic R. Honner DJ. Lowman HB,
May Thoms LD, Wells JA.
MET. 40, 1177 (A.S.)
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R24047;
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this sequence represents the light chain Fab portion of the 4D5 numerised to actionly list relighises the HERY2 receptor. The 4D5 decreases the HERY2 receptor. The 4D5 decreases the HERY2 receptor. The 4D5 decreases the Track list of plannid prints, which had the DNA encoding to the track to the content of the plannid was used to trackform.

und mit medisina insign prior to solgotion Nain 46; Fla II: 102pp: Enalish.

errothists to though was then used in a KiA for the HERY2 antigen

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helper phage having a gene vacching the phage confidence suitable for forming the transformed infected host cells under conditions suitable for forming transformed particles containing at least a portion of the plasmid and capable of transforming the host, the conditions being adjusted so that no more than a minor amount of phagemid particles display more than one copy of the foslor protein on the surface of the modification of the particles of second to be covarient bond of an amino acid in the substrate perfide of at least a portion of the phagemid particles (4) contacting the family of exposed phagemid particles with an affinity molecule, where
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            displaying poly-peptide(s) as coat protein fishing.

Example 11: Fig 11: Bipp: English.

The present invention describes a method for selecting novel polypeptide substrates. The method comprises: (a) constructing a replicable expression vector comprising a transcription regulatory element operably linked to a gene fusion: (b) mutating the vector at one or more selected positions within the social year thereby firming a family of related plasmids encoding substrate peptides: (c) transforming substrable host only inferting the transforming substrable host.
                                                                                                                                                                                                                                                                                                      98 ---WYGOKPOKAPKILLIYSASELYSGAVESPESGSFSGITTIITISSEGFETTYYOOGHY 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176 ALQSGNSQESVIEQESKDSIYSLSSILILSKADYEKHKVYACEVIHQGLSSPVIKSFNRG 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 TIEPIEGGGIKVEIKKIVAARSVEIFFRSDEGIKSSTASVVGILKMFYFREAKVIMKVDK 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 HUPLIFGGSIKVEIKHIVAAPSVEIEPPSDEGLKSSIASVVCLLNNEYPREAKVGWKVDN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 ALGSGNSGESVIEGESKRSTYSESSITIESKARVEKHKVYATEVIHGGISSPVIKSENRG 240
                                                                                                                                                                                                                           1 MKKNIAFILASMEVESIATNAYADIQMIQSPSSESASVGDPVIITGPSSGSIVHGIGAIY 60
                                                                                                                                                     1 MKKNIAFILASMFVFSIAINAYADIQMIQSFSSLSASVGLEVIIICERAGGE VN-TAVA- 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    415 Fab molecile expressed on a phagemid surface.
Human: growth hormone; hGH; phagemid particle: enzyme substrate:
fusion gene: phage profein coat.
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80.8%, Score 1440: DB 1: Length 237:
30.1%, Pred. No. 1.22e-98:
Vative 5, Mismatches 14, Indels
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WPI; 99-059058/05.
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Guery Match
Best Local Similarity 50.18,
Matches 218, Conservative
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US-441871.
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09-AUG-1991; U
03-DEC-1991; W
06-AFR-1992; U
30-APF-1993; U
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the affinity molecule has affinity for the amino acid residue having the modified covalent bond, and (h) separating the phagemid particles that the blind to the affinity molecule from those that do not bind. The selection method is used for identifying enzyme substrates. The present expension to present an 4D5 Fab molecule expressed on a phagemid surface from the configuration.

So Sequence 698 AA, Score 1440, DB 1, Length 698; Rath Authority 40 18, Prof. No. 1 220-98.

Search completed. Thu May 18 11.45:07 2000 Job time : 19 secs.

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SUMMARIES

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                                                                                                                                                                         61 LHWYLLKEBRELIYKVSNPFSGVPPFFSGSGSGTDFTLRISRVEAEDDGLYFCSQST 120
                                                                                                                                 Score 1510; DB 2; Length 242;
Fred. No. 4.72e-97;
17; Mismatches 13; Indels 0; Gaps
                                                                                                                      I MKKNIAFLLASMEVESIATNAYADIVMTQTPLSLPVSLGDQASISCRSSQSLVHGIGNTY 60
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01-MAR-1995
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STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: Callifornia
                                                   TOPOLOGY: Linear
GE 242 AA, 26430 MW, 332270 GN,
                                                                                                                                                                                                                                                                                                                                                                                                                           Suguence 56, Application US/08398612A Patent No. 5886070 GENEAL INFORMATION: GENEAL INFORMATION: APPLICANT: Doershuk, Claire M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Fong, Sherman
APPLICANT: Hebert, Caroline Alice
APPLICANT: Kim, Kyung Jin
APPLICANT: Leong, Steven R.
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INFORMATION FOR SEQ ID NOT 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 242 amino acids
TYPE: Amino Acid
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/398
FILING DATE: 01-MAR-1995
APPLICATION NUMBER: 08/205
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APPLICATION NUMBER: US
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 incl
                                                                               Query Match
Best Local Similarity 87.6%;
Matches 212; Conservative
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CORRESPONDENCE ADDRESS:
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GENERAL INFORMATION:
APPLICANT: Fong, Sherman
APPLICANT: Hebert, Caroline Alice
APPLICANT: Kim, Kyung Jin
APPLICANT: Leong, Steven R.
TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Ireatment of Inflam
NUMBER OF SEQUENCES: 58
CORPESPONDENCE ADDRESS:
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MEDIUM TYPE: 5 25 inch 360 Kb floppy disk
COMPUTER: 1BW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE. PATIN Genentech)
COPPUTER DELIN (Genentech)
APPLICATION DATA:
APPLICATION NUMBER: US/08/398,613A
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    ATTOREX JAEN TINGERMATION:
NAME: LOVE. RICHARD B.
PEGICSTPATION WIMBER: 94,659
REFERENCY/DOOKET NUMBER: P0874P1
TELECOMMUNICATION INFORMATION:
TELEFAX: 415,952-9881
TELEX 910/371-7168
INFORMATION POS ESC ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 242 amino acids
TYPE: Amino Acid
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CITY: South San Francisco
STATE. California
                                                                                                                                                                                                                                                                                          242 AA; 26430 MW; 332270 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 56, Application US/08398613A Patent No. 5677426
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03-MAR-1994
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                                                                                                                                                                                                                                                                                                                                                       Local Similarity 87.6%;
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FILING DATE.
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US-08-398-613A-56
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87.69, 8264, Mo. 4.726/97,
901,99, 17; Mismatches 13; Indels 0: Gaps
FILLNS LATE, J. MART1994
"IASSIFIANT" 435
FILL APPLICATION LATA
APPLICATION NUMBER: CQ/225804
ALTONICATE COMPRISE
ALTONICATE COMPRISE
ALTONICATE COMPRISE
NAME: FLAS, POLICO A
PRISTANTION NUMBER: 35,136
PRISEMBLENCY, COMPRISE
BELENCHMANNOATION INFORMATION:
BELENCHMANNOATION INFORMATION:
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Parest No. 570/2946
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TELEX: 310/771-7168
(NP.9MATITN POR REQ ID NO: 56: SENTENDE CHARACLEFAILS: 1 | 1 | 242 ambito artidis ITPE: abuno acid
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187 Loral Section 13,
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181 ALGSGNSGESVIEGDSKESTYSLSSTLILSKADYEKHKVYACEVIHGGLSSPVTKSFNRG 240
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APPLICANT: Henner, Dennis J.
APPLICANT: Henner, Dennis J.
APPLICANT: Greene, Ronald
APPLICANT: Greene, Ronald
APPLICANT: Greene, Henry B.
APPLICANT: Matthews, David J.
APPLICANT: Matthews,
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Best Local Similarity 87.5%; Fred. No. 4.726-97;
Matthes 212, Cliserrative 17, Mismatches 13, 1030);
MEDIUM INPE: 3.5 http., 1.44 Mt. 10449, dish COMPUTER: IBM PC COMPUTED COMPUTED COMPUTED COMPUTED COMPUTED COMPUTED COMPUTED CORRAIN SYSTEM: PC-DOS/MS-DOS CORRENT APPLICATION DATA:
ALLICALISATION NOMBER: 08/205864
FILING DALE: 03-MR-1994
ATTGENEY ASTRUT INFORMATION:
NAME: LOVE, RICHARD B.
REGISTRATION NOMBER: 34.659
RELEX: 910/371-7168
INFORMATION FOF SEG ID NO: 56:
SEQUENCE CHRRACIERISTICS:
LEUK: 910/371-7168
INFORMATION FOF SEG ID NO: 56:
SEGUENCE CHRRACIERISTICS:
LENGTH AMINO ACID
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5. Mismatches 14; Indels 5; Saps
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                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OFFRAING SYSTEM: PC_DOS/MS-DOS
                                                                                                                                              US/08/463,587A
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                    : 460 Foint San Bruno Blvd
South San Francisco
California
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                                                                                                                                                       FILING DATE: 05.7un-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER 08/050058
FILING DATE: 30.APR-1993
PRIOR APPLICATION DATA: 1993
APPLICATION NUMBER: PCT/US91/09
                                                                                                                         SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463.5
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REFERENCE/GGCKET NUMBER: FO IELECOMMUNICATION INFORMATION: TELEPHONE: 415/225-7467
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FILING DATE: 03-DEC ...
FILING DATE: 03-DEC ...
AITCHNEY/AGENI INFORMATION:
ACCOMMENTED, TIMOCHY R. SCHWARTEZ, TIMOCHY R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 25:
          Genentech, Inc
                                                                                                                                                                                                                                                                     FILING DATE: 09-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/71
                                                                                                                                                                                                                                                                                                        FILING DATE: 14-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/68
                                                                                                                                                                                                                                                                                                                                          FILING DATE: 10 APR-1991
PRICE APPLICATION DATA:
APPLICATION NUMBER: 07/62
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TYPE: Amino Acid
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
CORRESPONDENCE ADDRESS:
                                                        USA
            ADDRESSEE:
                                                                  94080
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                                           STATE:
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TILLE OF INVENTION: Enrichment Method For Variant Proteins
TILLE OF INVENTION: With Altered Binding Properties
NUMBER OF SEQUENCES: 27
COPPESPONDENCE ADDRESS:
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85.8%; Score 1440; DB 3; Length 237;
Best Local Similarity 90.1%; Pred. No. 4.88e-92;
Matches 218; Conservative 5; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 350 Kb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
237 AA
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     : Lad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                              Sequence 26, Application PC/TUS9109133 GENERAL INFORMATION: APPLICANT: Genentech, Inc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/US91/09: CLASSIFICATION: 425 PPIOR APPLICATION DATA: APPLICATION NUMBER: 07/743614 PRIOR APPLICATION NUMBER: 07/715300 PRIOR APPLICATION DATA:
                                                                                                                                                      Sequence 25, Application PC/TUS9109133
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/521657
ATTOPNEY/AGENT INFORMATION
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PEGISTRATION NUMBER: 30.445
PEFERENCE/DOCKET NUMBER: 645
TELEPHONE: 415/266-1489
                                                                                                                                                                                                                                                   Genentech, Inc.
Genrard, Lisa J.
Henner, Dennis J.
Bass, Steven
Greene, Ronald
Lowman, Henry B.
Wells, James A.
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AMINO ACID
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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11) THE PROPERTY TO A STANDARD OF THE PROPERTY OF THE STANDARD OF THE PROPERTY OF THE PROPERTY
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APPLICANT LOSWNAH, Bonry B.
APPLICANT WALLS, James A.
APPLICANT WALLS, James A.
APPLICANT WALLS, James A.
APPLICANT WALLS, BARCHWAY BENEVE PER VARIANT PROTEINS
FILE OF INVENTION, EMELSHEET MITH ALLERED RINGING PROPERTIES
FYNHERY PROPERTY. 6
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FULLY CATE: 0.0-DEC-1997
ATERNAYA 433 (N. 5860) N.
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TASSIFICATION: 435
BETT APPLICATION OATA:
APPLICATION NUMBER: US 09/050 658
PET IN ACTION OATA:
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FILINS DALE: 10-APR-1991
1919 APP FOATION SATA-
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APPLICATION NUMBER: US 97/743,614
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South San Francisco
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C'MPTTE: IAM PC COMPALIDIO
GERATIN: SYSTEM: PC-D/S/MS-20S
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... 5444598
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PRIOR APPLICATION DATA:
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FILING DAIL: 14-JUN-1
PRICE APPLICATION DATA:
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Z1P: 94589
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STREET: 46
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SENEPAL INFORMATION:
APPLICANT. Heary E. Lowman. Lendra 3. Eresta. Family F. Jardien, "Als LowerITILE OF INVENITOR. Improved Anti-ige Antibodies and Worhood of TITLE OF INVENITOR. Improving Polypeptides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 85.8%; Score 1440; DB 2; Length 247; Best Local Similarity 90.1%; Pred. No. 4.88e-92; Matches 218, Conservative 5, Mismatches 14, Indels 5; Gaps
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PEFERENCE/DOCKET NUMBER: 64584D1
TELEPHONE: (415) 225-1249
TELERA: (415) 225-1249
TELERA: (415) 452-9811
TELER: (415) 452-981
TELER: (4
                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
FENCE 237 AA; 25977 MW; 322792 CN;
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Patent No. 5994511
GENERAL INFORMATION:
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PEGISTRATION NUMBER: 39,044
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SIAIE: Californi
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Patest No. 5994511
GENERAL INFORMATION:
APPLICANT: HEAVEN B. Lowman, leonard G. Presta, Paula M. Jardieu, John Lowe IIILE OF INVENTION: Improved Anti-IgE Antibodies and Method of IIILE OF INVENTION: Improving Polypeptides
                                                                                                                                                                                                                                                                                          III EIREESSE IKSIAAVVOLLNATI KEAVVAMKUENALASSASGESVIEGESKESIVSI. 179
                                                                                                                                                                                                                                                                                                                                                                       144 FIFPPSDEQLKSGIASVVCLLNNFYPPPAKVQWKVPNALQSGNSQESVIEQDSKDSIYSE 203
                                                                                                                                                                                                                                                   1 DIQLTOSPSSLSASVGDRVTITCRASKP-VEGEGDSYLNWYQQKPGKAPKLLIYAASYLE 59
                                                                                                                                                                                                   14; indels 1; Caps
                                                                                                                                                                  Match 80.1%, Score 1345; DB 2; Length 218; Local Similarity 90.9%; Pred. No. 3.07e-85; ld. fonservative 5; Mismatches 14; Indels
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DUS/MS-FDS
SOFTWARE: Winhatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                 204 SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/US/847,3528
FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
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FPFPRENCE, NOWBER, F1123
IELECOMMUNICATION INFORMATION:
IELEPHONE: 650/225-1489
IELEFAX. 650/352.981
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
IYPE: Amino Acid
                                                                                                                             JOGY: Linear
218 AA: 23800 MW: 271099 CM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 19, Application US/08887352B
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IELECOMMUNICATION INFORMATION:
IELEPHONE- 650,7225-1489
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CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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                                                                                                                                           SEQUENCE
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Best Local :
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APPLICANT: Henry B. Lowman, Leonard G Presta, Paula M Jardieu. John Lowe TITLE OF INVENTION: Improved Anti-19E Antibodies and Method of TITLE OF INVENTION: Improving Polypeptides
CORPRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                             120 FIFPPSDBDLKSJANVVILLINNFYFPEAKVGWYVONAUGSSNSQESVJEQUSKISTYSI 179
                                                                                                                                                                                                                                                                                    60 SGVPSPFSGSGSGTUFTLIISSLÜPEUFATYYCQQSHEDPYTFGQGTKVFTFTVAAPSV 119
                                                                                                                                                                                                                                                                                                                144 FIFFPSEEQLKSSIASVVOLLNNFYFREAKVOWKVDNALÇSGNSQESVTEQDSKESTYSL 203
                                                                                                                                                                                                1 BIQLIQSPSSLSASVGDRVIIITGPASKP-VDGEGDSYLNWYQQKPGKAPKLLIYAASYLE 59
                                                                                                                                                        Gaps
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                                                                                                         Length 218;
                                                                                                       Query Match 80.1%, Score 1345; DB 2; Length 218 Best Local Similarity 90.9%; Pred. No. 3.07e-85; Matches 199; Conservative 5; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READBLE FORM:
MEDIUM IYPE: 3.5 inch, 144 Mb floppy disk
COMPUTER: IBM PC compatible
OPEDATING SYSTEM: PC-PAS,MS-DOS
SOFTWARE: WinPatin (Genentech)
CUPPENT APPLICATION PATA.
APPLICATION PATA.
APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-Jul-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         204 SSTLTLSKALYERHPVYAGEVTHGGLSSPVTKSFNPGFC 242
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                                              OGY. Linear
218 AA; 23800 MW; 271009 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: Linear
NOE 218 AA, 23800 MW, 271009 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 24, Application US/08887352B
Patent No. 5994511
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TELEPOMMUNICATION INFORMATION:
TELEPEAX: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO. 24
SEQUENCE CHARACTERISTICS:
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California
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NAME: SVODOda. Craig G
REGISTRATION NUMBER: 39.
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1: 218 amino acids
Amino Acid
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GENERAL INFORMATION:
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TS-08-987-3529-24
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                                              TOPOLOGY.
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  LENGIH:
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                                                                 SEQUENCE
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TILLE OF INVENTION: Anti-selectin antibodies for prevention of militie organisms of sequences: 4 corpressionnemer address:
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                                                           60 SOVESHESOSOSOIDETLITEST phane ATVENTED WHENCH FOR TEVETEVET KRIVAAPSV 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 SSTLILSKADVEKHKVYACEVIHOGISSPVIKSFNRGEC 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         204 SSILILSKALYERHRVYATEVHUSISSEVIKSENRGEC 242
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APPLICATION NUMBER: EP 95 114 969.9
FILING DATE: 19-Sep-95
ATIGNEY/AGENT INFORMATION:
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CURRENT APPLICATION DATA:
APPLICATION NUMFER: POL/HS96/13152
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ADDRESSE: Attn: Norman D. Hanson
SIREEI: 805 Ihiid Avenue
CIII. New York
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UENCE 218 AA; 23855 WW. 269234 CM:
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COMPUTER PEADABLE FORM:
WEDIUM TYPE: 3.5 Computer Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DGS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Martin, Ulrich, et al.
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APPLICATION NUMBER: 08,7578,953
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IELEFAX: (212) 838-3884
INFORMATION FOR SEQ 15 NO: 2:
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PTT-9896-13152-2 SIAMDARD:
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APPLICATION NUMBER: EP
FILING DATE: 17-Aug-95
APPLICATION NUMBER: EP
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LENGIH: 218
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STRANDEDNESS: single
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PEGISTRATION NUMBER:
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STATE:
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Howar Lord Simulating 97.98, Prod. No. 3.076-85.
Minister, Terr Transferring In Mismacobes 14: Indois In Gaps II:
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                                                                                                                                                                1 FIGHTOSPSSISASVOLPVTITTPASKP VEGESBATINWIGGROFAPEHLIYAASYLE 59
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Forth Similarity victory Prod. No. 3.076-85;
And This Pusoryation 5: Mismatches 14; Indels 1: Gaps
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POTENTIAL CONTRACTOR OF THE PATHECTOR OF PROBRESCO 242

PAGE SCHOOL AND TREASON A LIVER DESCRIBED TO THE PROBRESCO 242
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O'BRENT APPLICATION DATA:
APPLICATION TYMPIN- TO/F 8/997, FILE
FILLING LATE: 84-591-1997
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LENNIH 219 amico acids
TYPE: Amico Acid
TYPE: Amico Acid
TYPE: All Anico Acid
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CLASSIFICATION: 539
THREE ATTENT INFERANTINE
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APPLYANT HOLYS
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TS FR 947 3528 15
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NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Generatech, Inc.
SIREE: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                      SGIPSKESSSISSIDFILIISSLÜPEDFATYYÖLÜSNEDPWIFGLGIKVEIKRIVAARSV 119
                                                   44 SAVESPESISSISTEPTITIES LYPEDFATYYCS STHAPLIFORSTRAETKPTAAPSV 143
                                                                                         120 FIEPPSDEZIKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQNSKBSTYSU. 179
                                                                                                       24 DIGMIGSPESISASVODEVILICHSSOSLVHGIGAIYLHWYQQKPGKAPKILIYKVSNHF 93
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Score 1241: DP 1: Length 237:
Prod No 5 946-85:
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                                                                                                                                         SOFTWARE: WinPatin (Genertech)
CURRENT APPLICATION DATA:
APPLICATION NUMBEP- 15,708,798,511A
FILING DATE: 01-Mar-1995
CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                       Sequence 28, Application US/08398611A
Patent No. 5702946
                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Doershuk, Claire M. APPLICANT: FCL3, Sherman: PAPLICANT: Hebert, Caroline Alice APPLICANT: Kim, Kyung Jin APPLICANT: Leong, Steven R.
                                                                                                                                                                                                                                                                                                 Sequence 29, Application US/08398611A
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  TELEX. 415,952-9881
TELEX. 910,371-7158
INFORMATION FOR SEQ ID NO. 28:
SEQUENCE CHARACTERISTICS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/20
FILING DATE: 03-MAR-1994
AITORNEY/ASENT INFOFMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 01-Mar-1
CLASSIFICATION: 424
PRICE APPLICATION DATA:
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Best Local Similarity 81 4%;
Matches 197: Conservative
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MEDIUM TYPE: 3.5 inc
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                                                                                                                                                                                                                                                                                                                                     Patent No. 5702946
GENERAL INFORMATION:
                                                                                                                                                                                                          RESULT 13
ID #g-:9-348-611A-29
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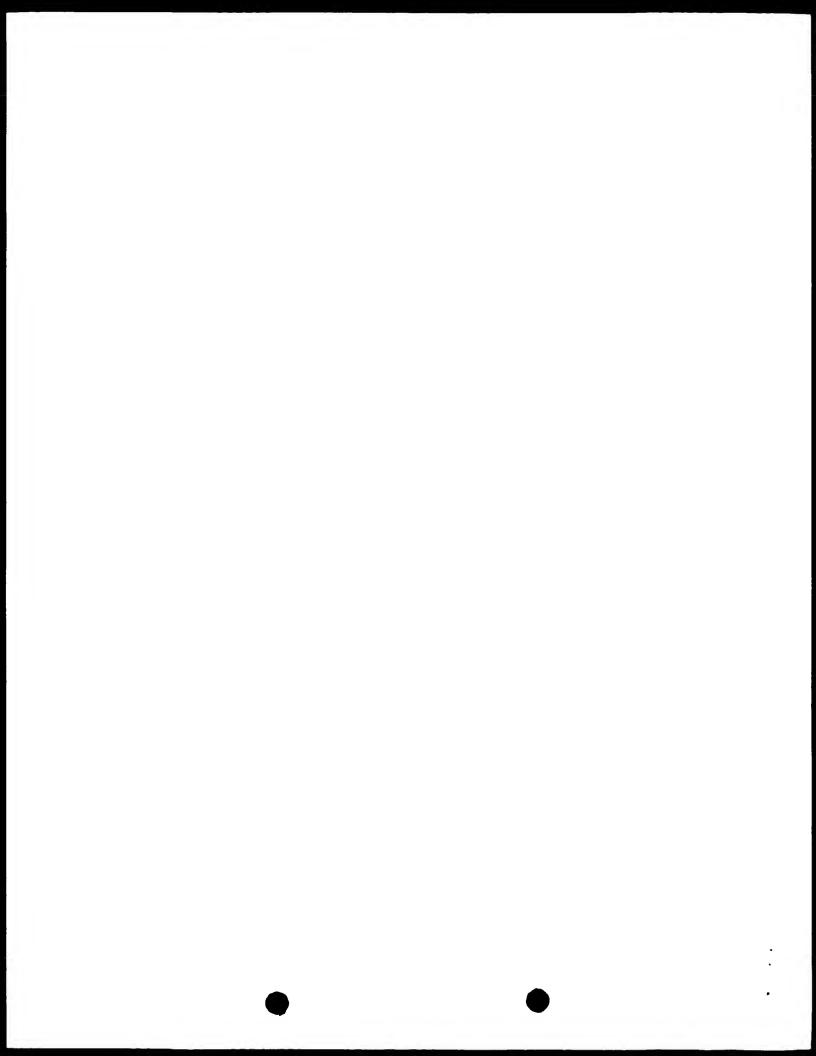
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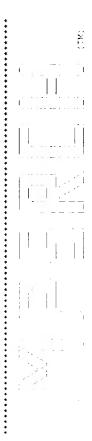
Mismatches 21.

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58 ---WYGREGSPRALIYSSSYRYSGVEDFFIGSGSGTDFILLTISHVQSFGTADYFGQQYN 115
                                                                                                                                                                                                                           121 HVPLTFGGGTKVEIKPTVAAPSVFIFPPSDEGLKSGTASVVCILNNPYPPFAKVQWKVDN 180
                                                                                                                                                                                                                                                                                                                            61 LHWYQQKPGKAPKLIYKVSNPFSGVPSPFSGSGSGTDFTLTISSLQPEDFATYYGSGST 120
                                                                                                                                                                                                                                                                                                  176 ALQSGNSQESVTEQDSKDSTYSESSTLTLSKAPYEKHKVYAGEVTHGGLSSPVTKSFNPG 235
                          1 MKKNIAFLLASMEVESIATNAYADIVMIQSQKEMSTSV3DFVSVICKASQN-V-GINVA- 57
                                                                                                                                                                                                116 IYELTEGPGTKLELFFAVAAPSVFIFFFSDEGLKSGTASVVCTANNFYFFEAKVQWKVDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Doershuk, Claire M
APPLICANT: Fong, Sherman
APPLICANT: Hebert, Caroline Alice
APPLICANT: Hebert, Caroline Alice
APPLICANT: Hebert, Caroline Alice
APPLICANT: Hebert, Caroline Alice
APPLICANT: Him, Kyun, Kyun, Ri, Kin, Kyun, Steven R.
TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for
TITLE OF INVENTION: Treatment of Inflammatory Disorders
NUMBER OF SEQUENCES: 58
COPPRESSOREMENT AND PRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       237 AA
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C.
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STREET 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
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Patent No. 5686070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Segmence 28, Application US,709399612A
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CURPENT APPLICATION DATA:
APPLICATION NUMBER US/08/398.6
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TELEX- 910/371-7168
INFOPMATION FOR SEQ ID NO-
SEQUENCE CHARACTERISTICS:
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GENERAL INFORMATION:
APPLICANT: Doershy
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ID US-08-398-612A-29
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APPLICATION NUMBER: 98733
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REFERENCE/DOCKET NUMBER: P0874P2
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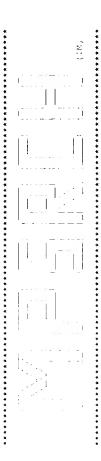
IE0242 #type complete Ig kappa chain NIG26 precursor - human #formal_name Hymo espient #common_nume nan 05-pec-1998 #sequence_revision 05-bec-1998 #text_change JE0242	JE0241 Alim, M.A.: Yamaki, S.: Hossain, M.S.: Takeda, K.: Koiima,	M.; Takashi, 1.; Shinoda. T. submitted to JiPID, November 1998	0	JEOSÁS Lype protein 1918 - 1918 - 1919 - 1919	#	<pre>ch 1 Similarity 82.2%, Fred, No. 4.29e-176, 180; Conservative 15; Mismatches 20; Indels 4: Gaps 2</pre>	ELVLIGSPGILSLSFGERATLSCRASGS V··SHHYLAMYQQKFGQAFSLLITAASARA 56 	STEBFESSSSTELLITSSLEFECFAVYZG-YDFFWHFT-SSTEVET WENTANARY 116	SOVESPESGSGSSIETTISSTOPETHAT TO THE TOTAL TO THE TOTAL TO THE TABLE TABLE TO THE TABLE TABLE TO THE TABLE	FIFFFSECLERGIASAVILLNEVPEAVYWWYNALGSANSJENTFGGGGTYSL 176	is posto, en esperant directant violetant, movement, en especiel especiel de 200	SSILILSKALVEKHRVVANJEVIHJOLG VIKEFNPOEC 115	STILIBRADYERHKVANGEVIHOUST SETVINGEN 2.2		JUSE44 #INTEG COMPLETE In Nathala MIND Promited (Compa	CONTROL OF THE CONTRO	. V.E.M. 1448 #Application Profession C. 1440 1948 #CCAC_Condition OS-Dec-1998
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Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata,
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A new subgroup of k type light chains (VkV) identified in
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                       F.; Yamaki, S.; Kazi, H.: Takashi, I.; Shinoda, T. submitted to TIPID, Normmber 1998
A new subgroup of K type light chains (VkV) identified acases of AL amyloidosis.
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#journal J. Biol. Chem. (1991) 266.2836.2842
#title The primary structure of the Fab fragment of protein KAU,
monoclonal immunoglobulin M cold agglutinin.
#cross-references WID:91131575
#accession A23746
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submitted to JipiD, November 1998
Structure relationship of kappatype light chains with Aliamyloidosis: Multiple deletions found in a VkIV protein.
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Pelease C.A. John P. Collius, Blocomputing Research Unit rightful: (c) 198-1998 University of Elukargh, J.K. distribution rights by Oxford Molecular Ltd out: The May 15 11.35.45 2000, Mastar time 121.32 Seconds Tabellar output not represented.

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                                                                                                                                                                                                                                                                                                                   19; Mismatches 14; Indels
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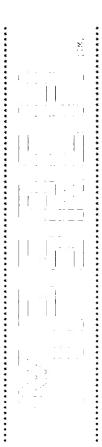
34 COMPLEMENTARITY-DETERMINING FRAMEWOPK 2.

55 COMPLEMENTARITY-DETERMINING 88 COMPLEMENTARITY-DETERMINING 97 COMPLEMENTARITY-DETERMINING 10,7 FRAMEWOPK 4.

84 SIMILARITY.

107 RAMEWOPK 4.

108 SIMILARITY.
                                                                                                                   PFAM; PF00047; 1g: 1.
Immunoglobulin V region: Monoclonal antibody; Hybridoma.
                                                                                                                                                                                                                                                                  12273 MW; F9F39CE949A84C2A CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 KAPPA CHAIN V-I FEGION 0U.
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HSSP, P01607; IREI.
PFAM; PF00047; ig: 1.
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Performer 3.1A John F. Collins, Riocomputing Research Unit. Copyright (Q) 1444-1449 Januarity of Ediabardh U.K. Listin rioca tinits by Oxford Mobellat Ltd.

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SUMMARIES

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01-NOV-1999 (ITEMBLE). 12, Last Sequence update)
PROTEIN ITEMSITE PROSPHARASE. NON-PECEPTOR TYPE SIRSTRATE 1 PRESTITEORS
(SHP SUBSTRATE-1) (INHITTORY PECEPTOR SHPS-1) (SHPS-1) (SIGNAL-
PECHLATORY PROTEIN ALPHA-1) (SIRP-ALPHA1) (MXD-1 ANTIGEN).
PIPNSI OR SHPS-1 OR DJ684024.1.
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"A family of proteins that inhibit signalling through tyrosine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 G-AG-AGRELIYNQKEGHFPRVTTVSELTKRNNLDPSISISNITPADAGTYYCVKFRKGS 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186 BRELYSYDEYINVYDEAGOSVSYSIHSJARVVIJEGDVHSZYVYJGETAHITE 223
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Prof. Mr. 5 Arn-25,
64, Mismatches 87, Indels 21.
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Liherla, Primates; Catarrhini; Hominidae, Homo.
                                                                                                                                                                     Bukaryota: Metazoa: Chordata: Craniata; Vertebrata: Mammalia:
Estheria: Primates: Catarrhini; Hominidae: Homo:
                                  GL-NOV-1999 (ITEMBLEEL 12, Created)
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CL-NCV-1999 (TEEMBLEEL 12, Last annotation update)
DISTSH24 2 (SIPP-RETAI (SIGNAL PEGULATOPY PPOTEIN RFTA 1))
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KHARITOMENKOV A., CHEM Z., STRES I., WANS H., SCHILLING I
                                                                                                                                                                                                                                                                            Commun. 231:61-67(1997)
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31-NOV-1998 (TTEMBLIFE) 08, Created)
51-NOV-1998 (TTEMBLIFE) 08, LASE SEGI
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Submitted (MAR-1999) to the EMBL/GenBank/DDBT databases
-!- FUNCTION. BINDS TO THE SH2 DOMAINS OF PROFEIN TYPOGINE PHOSPHAIASE
-ZC (SHP-2) AFTER TYPOGINE PHOSPHOPYLATION INDUCED BY VARIOUS
MIPOGENS AND JELL ADMESTION. MAY ACT AS A POCKING PROFEIN AND
INDUCE TPANSLOCATION OF SHP-2 FROM THE CYTOSOL TO THE PLASMA
                                                                                                -!- SUBCELLULAP LOCATION: TYPE I MEMBRANE PROTEIN.
-!- IISSDE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST LEVELS IN RRAIN.
HIGH LEVELS ALSO PRESENT IN HEAPT. SPLEEN, TESTIS, OVARY AND PERPHERAL BLOOD LEUKOCYTES.
-!- SIMILARITY: PELONGS TO THE IMMUNOSIOBULIN SUPERFAMILY. CONTAINS EMBL: D66043; BAA12974.]: -|
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                                                                                                                                                                                                                                                                                        Transmembrane: Alternative splicing; Immunoglobulin domain;
tein; SH3-binding: Phosphorylation.
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Pred No. 1 50e-24;
58; Mismatches 93; Indels 17;
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Eukaryota, Metazoa, Chardata, Craniata, Vertebrata: Mammalia;
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PHOSPHOPYLATION (POTENTIAL).
PHOSPHORYLATION (POTENTIAL).
PHOSPHOPYLATION (POTENTIAL).
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01-AUG-1999 (TrEMBLrel. 11, Last annotation update)
SIGNAL-REGULATORY PROTEIN BETA-1 PPREURSOR (STRP-BETAL).
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SH3-BINDING (POTENTIAL)
SH2-BINDING (POTENTIAL)
SH2-BINDING (POTENTIAL)
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IG-LIKE C1-TYPE DOMAIN.
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503 AA
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Mean 32.96%; Variante 181.740; scult 0.192

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SUMMARIES

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	1,676	1.63	242		W69302	ised anti-I	2.21e
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RESULT 1 ID W69302 standard; Protoin; 242 AA. AC W69302.	DI 15-FEB-1999 (first entry) DE Humanised anti-11-8 664V11N35E light chain.	KN Humanised artibody, monoclonal antibody, interlerving 8: via codvilate, actions immunochement, thereare, provincies	AN 004VIINSUB, INTIDAMEDICOL, IMMUNOCHMIDPY, CHERAPY, PROFILERSON, KW. inflammatory bowel disease, Crobe's disease, Northielle, (2011)	KW ischaemic reperfusion) adult respiratory distress syndrome:	KW dermatitis; meningitis; encephalitis; uveitis; autoimmune disease;	KW rheumatoid arthritis; Sjorgen's syndrome; "asculitis;	KW leukocyte diapedesis: multiple organ injury syndrome: septicuemia;	KW trauma; alcoholic hepatitis; pheumonia; pleurisy; alveolitis; vw dagan) (+) & byzyckitig byzyckitig two patitists.	os Chimeric - Homo sapiens.	OS Chimeric - Mus sp.	Synthetic.	Key Sonation/Qualifier	Peptide 123	/mare: sid_pertiage //note: "Siii leader perti	Region 4752	्य = [क्युक्ट]	/bote= "compressiarity determinas region Li	Region		Region	Tabel = 13	months a burnishing based for approximately the control of the control of		20 FEE 1538.	AN TANK	ZINEMENTANIA ZINEMENTANIA	TARE V Respective Total AR Press of Shallership			N=PSDE: VSSG/I.	hew conjugates of animonal inageners. Having considerly files. Non-proteinacenus polymer holeentes, particularly folyethylene.	glycol, for improving the residence to dieth of the second	CARDANI CO. TAN MAT. CARONER. DIMENTALIA. TENER IN THE BEST SOLED OF BOTH CARONER OF BURBANSERS BATES INTERNATIONS OF STATES.	(TI-9) antibody 604VIIN94F light chain variable region in an	BURNAMANAN SOO SEELEE EE E	1 59302 standard: Protein: 242 AA. 69302 standard: Protein: 242 AA. 69302 standard: Protein: 242 AA. 69302 standard: Conty) 5-FEB-1999 (first entry) 6404011035 included: containing a manifed antibody: concainable assistanced antibody: concainable assistanced antibody: concainable assistance antibody: solutions: concainable assistance antibody: concainable assistance and antibody: concainable and antibody: concainable assistance and antibody: concainable antibody: concainabl
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W inchamic according and the page in a constitution of the consti	MAY INTIDIONAL THROUGH BY THE PROPERTY OF THE PROPERTY OF THE PROPERTY BY THE	KW ischaemic reperfusion; adult respiratory distress syndrome; MR dematicis; meningitis; encephalis; uveitis; autoimmune disease; KW thematoid arthifis; Synged's Syndrome; vasculitis; Meningitis; encephalis; uveitis; autoimmune disease; KW thematoid arthifis; Monte dispetatis; premonal pleurisy allored; Syndrome; scholis; Configuration; Demandia pleurisy allored; Synthetic. Chameric - Homo sapiens. Synthetic - Homo sapiens. Chameric - Homo sapiens. Synthetic - Mus sp. 1. 23 FFT Key 26 FFT	MAY dematthes mentioned arthritis encephalitis uvetis; autoimmuno disease, manuful dematthes species at the matth of arthritis. Syndromer alcoholitis. KW fraumat alcoholitis syndromer asconditis. KR traumat alcoholitis mattiple organ injury syndromer septicaemia, traumat alcoholitis. KR traumat alcoholitis preumonia; pleuristy alvelitis: KR traumat alcoholitis mattiple organ injury syndromer septicaemia. Chimeric - Mus sp. Synthetic. Location/Qualifiers FI	KW Theumatoid arthritis. Storgen's syndrome; wasculitis: WW Jacksoft diapdesis: milible organ injery syndrome; septicuemia; WW Trauma; alcoholic hepatitis; pneumonia; pleutisy; alveolitis; WW Asimilia. Executivis. Executivists alveolitis; Chimeric - Mus sp. Schimeric - Mus sp. Schimeri	Was remained an appearant multiple organ injury synctrones sensitive transmistic between the displacements alcoholitis; brinchicits in the properties of the properties and the sensitive transmisters of the sensitive transmission of the sensitive	WW transactional according to Departitis; preumonia; plourisy, aiveolitis; was an according to Errochitis; brinchicis; predicts also be according to the accord	Chimeric - Homo sapiens. Chimeric - Mus sp. Synthetic. 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Tomplementatity determining region 1.3" 2.2cu. 20.0000000000000000000000000000000000	Jabel 13 LUSESTICHAD. JUDGET TO THE PROBLEM TO THE SHAPPING TO THE LESS TO THE STATE OF THE ST	1.19837210-AD. 27-PG2-1098. 20-FG2-1098. 20-FG2-1098. 20-FG2-1098. 21-FER-1997. US-66444. (GETH) GENERIECH INC. HSSI V, Kennells I. Irong SR. Presta IR Shahrakh Z. Sapata GA. WHY WA 45671. New Cofn.yaates of antibody fragments having covalently attaching professionerous spilyner collaborates by investigation of the profession of the residence time in the crimination. Claim 38: Fig 45: 228pp: English. Hists the amino acid sequence of bumanised anti-interlection. Claim 38: Fig 45: 288pp: English. Hists Sa the amino acid sequence of bumanised anti-interlection. Claim 38: Fig 45: 288pp: English. Hists Sa the amino acid sequence of bumanised anti-interlection. Claim 38: Fig 45: 288pp: English. Hists Sa the amino acid sequence of bumanised anti-interlection and which contains a sequence of the contains and which contains a sequence of the contains and which contains and which contains and which contains and	27.753-1508. 27.753-1508. 27.753-1508. 21.FEB-1997, US-604444. (GETH.) GENENTECH INC. HSelv., Koumenis I. Leury SR. Presta IR Stablockh Z. Zapata A. Wapt GRAFSELVAN. N-PSDR. V5501. NENEN V5501. New conjugates of actiledy fragments. having corabently attactor of professional polymer rolpenies, particularly polymer colpenies. New conjugates of actiledy fragments. having corabently attactor professional polymer rolpenies. particularly polymer colpenies. New professional polymer rolpenies, particularly polymer colpenies. New fragments for improving the residence time in the circulation. Claim 35: Fig. 45: 228pp. Endlish. Nis is the amino advantable deavel by maninged anti-interipering an interpretation. (II.9) antibody geavel light chair variable rodre an an H-cominal fusion with the XIII leader poption, and which contains and which contains and which contains and which contains and profession with the residence of the contains and particular colors.	20.F22.598; 003337. 21.ERB-1998; US-01116. 21.FEB-10. US-000444. (GEDH.) GENDWECH INC. HSeb V. Koumenis I. Leurg SR. Presia IR Shahrukh Z. Zapataa GA, WPI: da.4.6764740. N-PSDB: V55071. N-PS	21-1AN-1299 US-92116. 21-EB-1997 US-604444. (GETH) GENDWECH HO. HSEL V. Koumenis I. Leung SR. Presia IR Shahrakh Z. Zapata GA, WHI - GA-4-AFARAYA). N-PSDR: VS5071. New Coftyagates of actibility fragments. having curvalently stink non-proteinaneous polymer roleroles, particularly polyethylene glysch, for Improving the residence time in the circulation. Claim 25: Fig 45: 228pp: Endlish. This is the amino acid sequence the in the circulation. This is the amino acid sequence their valiable region in an History for Management and Sequence than the circulation.	ZIPERLUSS US-606444. (GETH.) GENDUTECHING. HSGIV, KOUMPDIS I. Leave SR, Presia IR Shahrukh Z. Zapara CA. WHIT GA 46764140. NEW COLG, GATERIA (1997) NEW COLG, GATERIA (1997	Habit V, Communication and SR, Presia is Shahrah Z. Zapata GA, Wall dwaffren,440. Neprose dwaffren,440. New Corp.ypates of antibody fragments having covalently attaction-profedements polymetry and antibody for improvation the residence than 16 th increments. Claim 38: Fig 45: 228pp: English. Claim 38: Fig 45: 228pp: English. Claim 38: Fig 45: 28pp: English.	Zapata GA, WPINE GA-46764,740. NEW COGN-95010 OF GALIED OF FROMENTS HAVING CONDIENTLY STITUTED OF PROPERTY POLYGENEE OF COGN-9501. NEW COGN-95010 OF IMPROVING THE RESIDENCE TIME IN the differentiation. Glasm 35: Fig 45: 32897 English of the differentiation. Glasm 35: Fig 45: 3289 English of the differentiation. (II.9) antibody 604VINN*F 1991 Chain variable region in an Nichemiaal fosion with the NIII Insder poption, and which contains.	WPIT 48.467687440. New Ordingstreet of antibody frequents having covalently attached ordinates versionally attached professional polymer unlamper, particularly polyethylene glycol. for improving the residence time in the differention. Classon 30: Fig. 9: 22889: Enables. Sistem 30: Fig. 9: 22889: Enables. Sistem antibody eachd segmence them warishle region in an Hereminal fosion with the NIII hader poption, and which contains.	N-PEGR, Vaccillately fragments— having covalently attached non-problematics of antibody fragments, particularly polyachylene olyace. For improving the residence time in the circulation. Claim 3: Fig. 4: 228pp. Enclish. Bits is the amino acid segmence in manised anti-precipition. Bits is the amino acid segmence in bimanised anti-precipitions (if a antibody GARVINASE 1994 chain variable region in an Hereminal fosion with the SIII leader poptide, and which contains.	her ordinadates of districts independs, particularly polyrebors, professionally polyrebors, polyrebors, particularly polyrebors, particularly polyrebors, profession, claim 25; Fig. 45; 228pp; Endlish. This is the amine add sequence of humanised anti-interletion; (i.e. a setting a sequence of humanised anti-interletions (i.e. a) antibody enable the Nicht onto an Ar-criminal fosion with the SIII leader period, and which contains and which contains.	glycol, for improving the residence time in the circulatio claim 35: Fig 45: 228pp. Endlish: lbis is the antic acid seguence of humanised anti-interle: (if-8) antibody 604VINN*F light chain variable region in Hereminal fosion with the SIII leader peptide, and which	this is the amino acid sequence of humanised anti-interied (if -0) antibody 604V11N°FF 11ght chain variable region in H-remminal fusion with the SIII leader period, and which	(II.e) antibody scavillast light chair variable region in W. corminal fusion with the STII leader peptide, and which	Marchael fusion with the STIT leader peptide, and which		

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the complementarity determining regions (CDRs) of murine anti-IL-8
antibody 634.2.5 (see W69309) light chain within a human 6-subgroup
I light chain template. Humanised anti-IL-8 monoclocal antibodies
(MAbs) and variants are described for use in diagnostic applications
and in the treatment of inflammatory disorders. The invention
provides conjugates of an antibody fragment and a non-proteinanceous
polymer such as PEG, that have improved half-life, mean residence
time, and/or clearance rate compared to non-derivatised parental
antibody fragment. Also claimed are a polypeptide that is an
anti-IL-8 MAb or antibody fragment comprising a light chain amino
and sequence comprising the light chain CDRs of 6G4V11N35E, a
nucleic acid encoding such a polypeptide, and a method of producing
the polypeptide in host cells. The conjugates can be used for
immune therapy of inflammatory disorders, e.g. psoriasis, responses
and ulcerative colitis), ischemic reperfusion, adult respiratory
distress syndrome, dermatitis, menhaditis, anothers,
autoimmune diseases such as rheumatoid atthribis, sirgen;
autoimmune diseases such as rheumatoid atthribis, sirgen;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Syndrome, vasculitis, diseases involving leukocyte diapedesis, central nervous system inflammatory disorder, multiple organ injury evndrome secondary to septicaemia or trauma, alcoholic hepatitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bacterial pneumonia, antigen-antibody complex mediated diseases, inflammations of the lung, including pleurisy, alveolitis, seculitis, pneumonia, chronic bronchitis, bronchiectasis, and cystic fibrosis. They can also be used in diagnostic applications. Sequence 242 AA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   th (Similarity 99.0%) Score 1676, DB 1, Length 242; Similarity 99.0%; Fred. No. 2.21e-117; 241; Conservative 1; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                syndrome secondary to septicaemia or trauma, alcoholic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers 439. .1167
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Best Local (
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W09837200 - A2

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Example K, Fig 418-D; 328pp; English.

This is the amino acid sequence of a polypeptide encoded by risamid p64V1N35A.F(ab')2 (see V4453) comprising a murine-human confamining complementarity determining regions of murine arti-interleukin's (11-8) monolonal antibody (MAb) 5:52.53 (see W6309-10) in a human template. Humanised anti-IL-8 MAbs (see W6309-10) in a human template. Humanised anti-IL-8 MAbs (see Conjugates of an antibody fragment and a polymer, such as PEG, that chave improved half-life, mean residence time, and/or clearance rate. The conjugates can be used for immune therapy of e.g. psoriasis, responses associated with inflammatory bowel disease (such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 LHWYQQKPGKAPKLLIYKVSNRFSGVPSPFSGSGSGTDFTLTISSLQPFDFATYYCSQST 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 HVPLIFGQGIKVEIKRTVAAPSVFIFPPSDEQLKSGIASVVCLLNNFYPRFAKVÇWKVDN 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKKNIAFLLASMFVFSIATNAYADIQMTQSPSSLSASVGDFVTITCPSSQSLVHGIGATY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Crohn's disease and ulcerative colitis), ischemic reperfusion, adult respiratory distress syndrome, dermatitis, meningitis, necephalitis, uveltis, autoimmune diseases such as rheumatoid arthritis. Sjorgen's syndrome, vasculitis, diseases involving leukocyte diapedesis. Sentral nervous system inflammatory disorder, multiple organ injury syndrome secondary to septicaemia or trauma, alcoholic hepatitis, bacterial pneumonia, antigen-antibody complex mediated diseases, inflammations of the lung, including pleurisy, alveolitis, vasculitis, pneumonia, chronic bronchitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Humanised anti-TL-9 664.2.5V1N35A light chain.
Humanised anti-TL-9 664.2.5V1N35A light chain.
Humanised anti-TL-9 664.2.5V1N35A light chain.
Humanised antibody: monoclonal antibody; interieukin-8;
f64.2.5; inflammation: immunotherapy; therapy; psoriasis;
inflammatory bowel disease, Crohn's disease; ulcerative colitis;
ischaemic reperfusion; adult respiratory distress syndrome;
dermatitis; meningitis; encephalitis; uuctimmune disease;
rheumatoid arthritis; syndrome; vasculitis;
leukocyte diapedesis; multiple organ injury syndrome; septicaemia;
                                                                                                                                                                                                      New conjugates of antibody fragments - having covalently attache\overline{\mathtt{d}}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bronchiectasis, and cystic fibrosis.
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                                         2.JAN-1998; US-012115.
                   003337
                                                                                                                                                                                N-PSDB; V44953
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This is the author of sequence of Eumanised anti-Interleukin-8 (11-9) antitody 664.2 5 ViNN35A light chain variable region in an (11-9) antitody 664.2 5 ViNN35A light chain variable region in an interpretation and which contains the complementary determines the complementary determines the complementary determines the following following following following following following the following antition of the following following antition of the following 
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// 35.64. 3 .re 1675. 36 1. Longth 242.
// 4.64. Simplarity (1.6%) eved, No. 2 (4e 117.
// 241. Subsequetion or Mismatches 1: Indels 0: Gaps.
trimus iloobolis hepatitis, promodaa, pleurisy, alveolitis, osa kiito, tronolitis, bromiliostasia, opstir fittisis, diaya sis
chimorio e Homo saplens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unites of antibody transpents is having covalently attached
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the preference of the residence time in the circulation. Alymphylene of the improving the residence time in the circulation. Claim 45; Fig. 36; 324pp; English.
                                                                                                                                                                                                                                                                                                             "respicachtarity determining region 11"
                                                                                                                                                                                                                                                                                                                                                                      /label* 12
//oto "remplementarity determining region L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "complementarity determining region 13"
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                                                                                                                                                                                                Class Sig_Fortile
                                                                                                                                    A STATE AND A STATE OF
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LZ 'AN 1998, 73 JIZ116.
J1 PER 1997; PS-894444.
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                                                                                       N. C. S. M.
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                                                                                          Spirit Service
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Monotonial anticody specific for interlanging a used for treating IL-8 mediated inflammatory diseases, e.g. ulcerative colliss in San-Baranes Fig 52A-By 63pp; English.

Else commerces Fig 52A-By 63pp; English.

This is a chimeric Fab 634-55 comparished of complementally determinant regions (1289) of a light obtain constant region of the human immunosiobalia [46]. This chimeric Fab is used to construct a plasmed programmer which consists of mutine-fannar variable-violater regions of both the light and heavy chains of 634-2.5 by various standard recombinant techniques. The activity and can inhibit the IL-8 binding to human neutrophils. This activity and can inhibit the IL-8 binding to human neutrophils. This amin inflammatory diseases and in the treatment of ulcerative collits and inflammatory diseases and in the treatment of ulcerative collits and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "o mplomostatity Actorations confined. Determined by X may crystallography"
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-- " work becoming determining region I. determined by X-ray crystallography"
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by X-ray orystallography"
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111 HVPLIFOGGIKVEJKETVAASSVEJFFGŠTOGL FGJJASVVILLMATTEJASVINGKEVIKSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W33745;
01-MAY:1998 (first entry)
Chimeric and interpretable (554.2.5) light chain .
Chimeric and interpretable chair . 654.2.5 light chain .
morrorlonal antibody. diagnosis: inflammatory disorder: treatment:
pneumonia, complementarity determining region: CDR; variable region:
constant region; chimeric: p65425chim2: ulcerative colitis.
Chimeric - Mus. Sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /notes- "murine light chain variable region"
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Deerschik CM, Feng S, Hebert CA, Kim KJ, Leong SR:
WPI: 98-076425/07.
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03-MAP-1994; US-205854.
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31-MAR-1995: 398611.
31-MAR-1995; US-3986
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                                                                                                                                                                                                                                                                                                                                                                               61 LHWYLOKPGUSPKLLIYKVSNRFSGVPDRFSGSGGTDFILRISRVEAEDLGLYFGSGST 120
                                                                                                                                                                                                                                                                              121 HVPLIFGAGIKLELKRAVAAPTVFIFPPSSEQLKSGTASVVCLLNNFYPREAKVQWKVDN 180
                                                                                                                                                                                                                                                                                                                    HVPLTFGGGTKVFIKPTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN 190
                                                                                                                    1 KKKMIAFLLASMEVESIATNAYADIVMIQIFLSLFVSLGDQASISGRSSQSLVHSIONIY FQ
                                                                                                                                                          1 MKKNIAFILLASMFVFSIATNAYADIQMIQSPSSLSASVGDRVIIICRSSQSLVHGIGETY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "complementarity determining region (CDR) as indicated by Kabat sequence comparision"
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                                                                                                                                                                                                                       191 ALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "complementarity determining region (CDR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117. .125
/note= "complementarity determining region (CDP)
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                                        Length 242
                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "murine variable light region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "human constant light region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "complementarity determining
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                                   Score 1511; DB 1; Pred. No. 1.38e-104.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            II 5
W42929 standard: Protein: 242 AA
W42923;
                                   Query Match
Best Local Similarity 87.6%,
Matches 212, Conservative
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03-MAR-1994; US-205864.
(GETH ) GENDUTECH INC.
(IND ) UNIV INDIANA.
Doptsobur CM. Forg S. Heb
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Chimeric - Homo sapiens.
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1-MAK-1995; 398512.
242 AA
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Treatment of bacterial pneumonia - with monoclonal antibody specific but interleukin 8; inhibits lung inflammatory conditions

Discipators, Fig 27, 63ps; Banlish.

The present sequence represents the sequence for murine monoclonal antibody 64.2.5 light chain variable region and a human light of interleukin 8 (10-8) antibody fole is an antil rabbit for interleukin 8 (10-8) antibody IL-8 is an antil rabbit contaction of interleukin 8 (10-8) antibody IL-8 is an entrophil chemotactic pertide secreted by a variety of cells in response to inflammatory mediators. IL-8 can play an important role in the pathogenesis of inflammatory disorders such as adult response to inflammatory and annihip cogar failure Treatment of baccerial pneumonia in a mammal comprises administering an antib in response to include to 10-11 M, inhibits neutrophil chemotaxis in response to bind to C5s, beta-16 or platelet factor 4. IL-8 specific monoclonal antibodies are especially for treating pneumonia caused by Streptococus pneumoniae. E. coli or Pseudomonas aeruginosa in humans. The antibodies may also be used in the treatment of ulcerative colitis and other infilammatory conditions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 ALQSGNSQESVTEGDSKESTYSLSSTLILSKADYEKHKVYACEVIHQGLSSPVIKSFNRG 240
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Chimeric 6G4.2.5 light chain.
Mcnoclonal antibody 6G4.2.5, MAb, interleukin-8, IL-8,
chimeric antibody; Fab; antibody engineering; inflammation;
inflammatory bowel disease: ulcerative colitis; bacterial pneumonia.
Chimeric Mus sp.;
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years Times location determined by Kabat sequence comparisons amino acids 78-80 constitute to the locations of the location of
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/ "..."TF ? ...attl.n Jetermined by Mabat.
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(6ETH ) GENENIECH INC.
(HDV ) CHIV INCIANA FOND.
FORTSCHOLD TO, FOND S. HOLDOEL CA. Kim KI, Loong SP:
WPI: 95-42-59024.
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Fragments of antibody to human interlevkin-8 comprising light and/or leavy chain sequences; used to prevent interlevkin-8 mediated neutrophil chemotaxis
Discissure; Fig 27A-B; 63pp; English.
This is a chimeric tab 534-2 comprising of complementarity determining regions (CDFs) of a light chain variable region of the nurine species and light chain constant regions of the numeric tab secies.

Affice: Fig. 1s sell: Missing a plusmid political with consists of murine-human variable/constant regions of both the light and heavy chains: 6 42-2 by carious standard recombinant techniques. The recombinant human-murine chimeric Pab has anti interlevent interlevent while anti-8 facility is sellicity to the treatment of bushing themosphile chemotaxis which is used to prevent interlevent of incrinity undistrible demogratis
                                                                                                                                                                                                                                                                                                                         /note= "complementarity determining region 1; determined
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/noie* "complementarity determining resion 3: deferming
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47. .62
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Best Local Similarity 87.6%: Pred. No. 1.386-104;
Matches III, Conseination IP, Mismaithes II.
1. .13
/coie= "signal peptide of STII"
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Fong S, Hebert CA, Kim KI. Leong SR;
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Methods for treating asthma in mammals with interleukin-8 (IL-8) antaqonists (anti-1L-8 antibodies) have been produced. Murine 664.2.5 microbial antibody is an anti-1L-8 antibody. The present sequence represents the murine 664.2.5 variable light chain region and the imman 1961 constant light chain region chimeric monoclonal antibody. Anti-IL-8 antibodies are especially used to treat or preparent altergic asthma in humans. They ishibit: (a) recurrethil chemicaxis in respecte to IL-8 mediated release of elastase from neutrophils and (c) binding of IL-8 to meutophils. Anti-IL-8 antibodies can be used to treat many other inflammatory disorders, e.g. isohaemic reperfusion. APDS, dermatitis, particularly bacterial pneumonia and inflammatory bowel
                                                                                    03-NOV-1997 (first entry)
Chimeric monoclonal antibody light chain region.
Interleukin-8, II-8; antagonist; anti-interleukin-9 antibody; asthma:
inflammatory disorder, neutrophil chemotaxis; elastase release;
ischaemic reperfusion, ARDS, dermatitis; bacterial prounchia;
inflammatory bowel disease; mouse; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /iabel= CDR_#1
/note= "According to Kabat sequence comparison"
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Pred. No. 1.38e-104;
18; Mismatches 12; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .abel = Murine_664.2.5_variable_light_chain
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/label= Human_IqGl_constant_light_chain
                                                                                                                                                                                                                                                                                                                                                                 Chimeric-Homo sapiens.
Rey Location/Qualifiers
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Hebert CA, Kabakoff RC, Moore MW;
WPI: 97-118712/11.
JI 8
W22790 standard; Protein; 242 AA
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24. .137
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/label= CDR_#3
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26-JUN-1996; U11033.
27-JUN-1995; US-491334.
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81 LEWELLARBOASERLLIYRVSNEESSYFCEESSSSSCTCFTIFTSFVEAFOLGLYFTSSST 120

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Immunotherapy of ulcerative colitis - with monoclonal antibody specific for interleukin-8
Example B: Fig 27: 63pp: English.
This sequence represents the light chain of a chimeric monoclonal antibody (Mac) composed of murine Mac 664.2.5 variable light chain and a human constant light region. This Mat is used in a novel method for
                                                                                                                                                                                                                                                            03-JUN-1998 (first entry)
03-JUN-1998 (first entry)
Chireric Mab 664 25 protein light chain.
Monoclonal antibody: Mab 664.2.5; interleukin-8; IL-8; murine;
ulcerative colitis; immunotherapy, bacterial preuminia, variable region:
treatment; light chain; heavy chain; neutrophil chemotaxis inhibitor;
constant region; human.
          61 LHWYQQKPGKAPKLLIYKVSNRFSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCSQST 120
                                      121 HVPLTPGAGTFLELKPAVAAPTVFTFPPSSEQLKSGTASVVCII.NNFYPPEAKVQWKVDN 180
                                                                                              191 ALQSGNSQESVTEQDSFDSTFSLSSTITLSKADYBKHKVYACEVTHQGLSSPVTKSFNPG 240
                                                                                                           121 HVPLTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN
/note= "alternative complementarity determining
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/note= "alternative complementarity determining
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138. 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "complementarity determining region #1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "murine variable light region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "human constant light region"
                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= 6G4.2.5_heavy_chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GETH ) GENENTECH INC.
Fong S, Hebert CA, Kim KJ, Leong SR;
WPI; 98-100296/09.
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W40126 standard, Protein, 242 AA.
W40126;
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01-MAR-1995; US-396851.
03-MAR-1994; US-205864.
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The distriction of the control which involves the administration of an unit II. A monocoust and body capable of binding to human interleuking (II.A) with a Kd of I.A to 10.10 K. This Nab also inhibits neutrophility of control inhibits in response to II.8, inhibits II.8 mediated elastase release by antirabilis and does not bind to 50a, but a 'IS or platelet factor 4, the unithelies and also be used for the treatment of bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 LHWYLUKPGDSPKILIYKVSNPESGVPDPFSGSGSGIDFILKISPVEABDLGLYPGSGST 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 HVPLIFGAGTKLELKRAVAAPIVEIEPPSSEÖLKSGIASVVCLLNNFYPREAKVQWKVDN 180
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Zover Templementarity determining region
determined by Xitay crystallegraphy"
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Assas "supplementarity determining region
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18: Mismatches 12: Indels
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/aote* "STII signal"
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orai Similarity 87.68,
s 212: Consormati
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Matches
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This chimeric polypopulae comprises the light chain variable region of finith and the west of the first chair the set of first chair the set of first chair the set of first chair the pulphpeptide has been utilized in the construction of first chair the pulphpeptide has been utilized in the construction of first chair the set of first chair the set of first chair the set of the s
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Pred. No. 1.38e-104:
Transcribes 12: Indels 0: Saps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New conjugates of antibody fragments - having covalently attached transfers particularly pulyerhylore glycol, for improving the residence time in the circulation.

Example F: Fig 27A-B: Right: English.
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/label= Complementarity determining region
determined by Rabat sequence comparison.
determined by X-ray orystallouraphy"XX
                                                                                                                                                                                                      /note= "complementarity determining region determined by X-ray crystallography"
                                                                                                                                                                                                                                                                                                                                 /note= "human constant light region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC.
Hsei V, Koumenis I, Leong SR, Presta LR, Shahrokh 2,
                                                                                                                                                                                                                                                                   139. .242
/label- Constant
                                                                                                                                                                               /label- CDR3
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Best Local Similarity 87.6%;
Matches 212; Conservative
                         .125
                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-JAN-1998; US-012116.
21-FEB-1997; US-804444.
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N-PSDB: V44951.
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/label= signal

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New stable agueous antibody formulations - comprising an antibody not subjected to lyophilisation, a buffer maintaining the pH at 4.5 - 6. a surfactant and a polyol bisclosure: Fig 21A. 87pp. English.

Disclosure: Fig 21A. 87pp. English.

The sequence is that of the pS1130 encoded light chain of a humanized murine anti-CD18 antibody rhuMAb CD18. It can be used for the treament of discorders which include haemorrhagic shock, thermal injury (such as that resulting from burns), stroke (including ischaemic and haemorrhagic stroke) and myocardial infarction. The antibody formulation can be stabilised at a temperature of 30 deg. C for at least one year or at a temperature of 30 deg. C for at least one year or at a temperature of 30 deg. C for at least one mouth and is stuble following incozing and thawking.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 12 W30534 standard; protein; 237 AA. W30534 standard; protein; 237 AA. W30534 (first entry) 6-APR-1999 (first entry) 8-Combinant humanised anti-CD18 antibody; rhuMAb CD18 light chain. Recombinant humanised anti-CD19 antibody; rhuMAb CD18; leucine dipper; murine monoclonal antibody; muMAb H52; protein recovery; filtration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 HVPLTFGQGTKVETKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVOWKVDN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56 LNWYQQKPGKAPKLLIYYTSTLHSGVPSPFSGSGSGTDYTLTISSLQPEDFATYYCQQGN 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 LHWYQQKPGKAPKILIYKVSNPFSGVPSRFSGSGGTDFTLTISSLQPEDFATYTGSQST 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 ILPPIFGQGIKVEIKRIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176 ALGSGNSGESVIEGDSKESIYSLSSILILSKADYEKHKVYACEVIHQGLSSPVIKSFNRG 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saps
                                                      C8-JUN-1999 (first entry)
pS1130 expression cassette encoded rhuMAb CD18 light chain
pS1130 expression cassette encoded rhuMab cD18 light chain
procession antibody beary chain, humanized; myccardial infarction;
burns; thermal injury; Ischemic, shock; ischaemic, hammorrhagio; stroke; light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87.0%; Score 1462; DR 1; Length 237; 90.9%; Pred. No. 8.53c-101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                           Ongpipattanakul B, Shahrokh Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Mismatches
                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                  W95622 standard; Protein; 237 AA.
W95622;
                                                                                                                                                                                                                                                                                                                                                             Lam XM, Oeswein JQ, Ongpipattane
Wang SX, Weissburg RP, Wong RL;
WPI, 99-080866/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    220, Jonsérvative
                                                                                                                                                                                                                                                                          17-DEC-1998.
12-JUN-1998; U12209.
13-JUN-1997; US-874897.
                                                                                                                                                                                                                                                                                                                                         (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chromatography
                                                                                                                                                                                                                                    Sig_peptide
W09856418-Al.
                                                                                                                                                                       Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           236 EC 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 EC 242
                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                           Lam XM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus sp.
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RESULT
                                        90
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Name that the recovering polypeptides from cell cultures - by treating with reagent and filtering to remove reagent treating with reagent and filtering to remove reagent treating with reagent and filtering to remove reagent to the reagent and filtering to remove reagent to the reagent accomposition comprising a polypeptide to a reagent which binds to modifies the polypeptide, where the reagent to make a man form a cold phase; and (b) passing the composition through a filter hearing an opposite charge to the reagent so as to remove leached reagent from the composition. The present invention also describes a method for modifying a precursor antibody to appreciate also describes a method for modifying a proteins from cell cultures. They are especially useful for isolating antibodies. The methods can be used to purify antibodies. The methods can be excluded from the protein as is the case in prior art immobilized modification systems. By using a opposite charge filter the reagent can be excluded from the sample, preventing concamination. The present sequence represents the reagent can be excluded from the sample, preventing concamination. The present sequence represents the reagent can be excluded from the case in prior and the present sequence represents the reagent can be excluded from the sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-JAN-1999 (first entry)
Protein encoded by Fab-display antibody vector phMB4-19-1.6.
Murine, humanised antibody VEGF-induced anglogenesis; tumour
anti-vescular endothelial growth factor antibody; anti-VEGF antibody,
retinal disorder; age-related macular degeneration; diabetic retinopathy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 LHWYQQKPGKAPKLLIYKVSNRFSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCSQST 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 HVPLIFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCIJANFYPREAKVQWKVDN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKKNIAFLLASMFVFSIATNAYADIQMTQSPSSLSASVGDRVTITCRASQD----INN-Y 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5, 3aps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKKNIAFLLASMFVFSIATNAYADIQMTQSPSSLSASVGDRVIITCRSSQSLVHGIGETY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 TEPPTFGGGTKVEIKRIVAAPSVEIFPPSDEGLKSGTASVVCLLNNFYPPEAKVGWKVDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176 ALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  II, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           which is used in an example from the present invention.
Sequence 237 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1462; DB 1; I
Pred No. 8.63e-101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lowman HB, Presta LG, Wells JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Mismatches
                                                                                                                                                                                     (PETH.) GENEWIECH INC
Blank GS, Narindray DS, Zapata GA;
WPI; 99:060267/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W70703 standard; Protein; 237 AA.
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Local Similarity 90.9%;
es 220; Conservative
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7-APP-1998.

7-APC-1997.

7-APR-1997; US-938469.

7-APR-1997; US-833504.

GETH) GENRYTECH INC.

Baca M. Chen YM, Lowman F

WPI; 98-568337/48.
                                                                                                                                                        13-JUN-1997; US-050951.
                                                                                                             12-JUN-1998; U12334
                                                                                                                                                                                                                                                                                                                    N-PSDB; X03840
                                      WO9856808-A1.
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Wogg45331-A2.
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241 EC 242
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Best Local S
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Example 3 Fig 80. E. 199pp. English.

Example 4 Fig 80. E. 199pp. English.

English intiled which is used in the course of the invention. The service interest of the invention discretes interested antibodies. The humanised antibodies are used in the humanised antibodies are used in a controlled in the Vent induced angiogenesis, particularly for treating are preventive to the total disorders (e.g. age for invention in the mount of the invention of the inventio
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This sequence represents the light chain Fab portion of the 465 communised of in Interval and the 455 communised of into the plasmides in Which had the town energy in the plasmid ps/152, which had the town a communication of into the plasmid ps/152, which had the town encoding from it was trown to income the first into the plasmid was used to transform by contrast in the plasmid was used to transform
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517 TOTALL LOTTELLE HELLELLE HELLE HEVYALGEVER GESTUTLESFALVELE HEVYALGEVER GESTUTLESFALVELE HEVYALGEVER GESTUTLESFALVELE HEVYALGEVER HELLE HEN HELLE HEVYALGEVER GESTUTLE HENDE HELLE HEVYALGEVER HELLE HENDE GESTUTLESFALVELE HEVYALGEVER HELLE HELLE HELLE HENDE GESTUTLE HENDE HELLE HENDE HELLE HELLE HENDE GESTUTLE HENDE 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54 LNWY J26FORARELLIYETSELESSYPSPESSSSILIYILIISSLQPEDEAIYYOQQYS 115
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New beganised antibuty with affinity for vascalar endothelial growth tarter ton treatment of tamours, retinal disease and other annionents states and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 I MAKNIAFILLASMEVESIATNAYADIGMTQSPSSLSASVGDPVTITGPSSQSLVHGIGETY 60
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Light chair of 40% East 100 and 1503y or recognises HDB-2 receptor.
Equations (fit antibody: Franch Growth Notwone: NGH; selection)
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es 219; Conservation 9; Mismatches 9; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Server has and entrained variant proteins comparises fusing der
entrained on arowal formton to part of ML3 phage coal protein
under the Fig. 12 (12) page Entrief to selection
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Sementer
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8-101, Wells JA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                s
P24°47 standard: Protein: 237 AA.
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MATTEMAS 10, WOLLS AND
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displaying polypeptide substants.

Stample 11: Fig 11: 81pp: English.

Example 11: Fig 11: 81pp: English.

The present invention describes a method for selection cover polypeptide of the present invention describes a method for selection a replicable construction a replicable of the selection selection of the present operably of the present operably of the present operably of the selection which the plasmids attanscription required to one or more selected plasmids encoding selected believed to one or more selected plasmids encoding selected believed to the present of describing the vector of one or more selected plasmids encoding selected believed to the plasmids and the polyment plage of the plasmids. (d) infection the transformed host cells with a cells with the plasmids acceptable under the plasmid particles of the transformed infected best cells under conditions situable for forming recombinant phagemid particles of the particle of the particles of the particle of the particles of the particles of the particle of the particles of the particle particle of the particle particle of the particle particle of the particle particle of the particle particle of the particle particle particle of the particle pa
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Human, growth hormone: hGH: phagemid particle: enzyme substrate:
fusion gene, phage privato clat.
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                                                           Length 237;
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WPI; 99-059058/05.
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                                                     Query Match
Best Local Similarity 90 18-
Matches 218: Conservative
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30-APR-1993; US-050058.
05-APR-1995; US-418928.
16-WAY-1995; US-41871.
(GETH.) GENENTECH INC.
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US-683400.
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09-AUG-1991; US-743614.
03-DEC-1991; WO-U09133.
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237 AA:
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the affinity molecule has affinity for the amino acid residue having the modified covalent bond: and (h) separating the phagemid particles that bind to the affinity molecule from those that do not bind. The selection method is used for identifying enzyme substrates. The present sequence represents an 4D5 Fab molecule expressed on a phagemid surface from the
                                                                                                                                                                                Shore 1437: DR 1; Length 698;
Pred No 7,44e-99;
5; Mismatches 14; Indels 5; Gaps 3;
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                                                                                                                                                                                                                                                                          Search completed. Thu May 18 11:53:53 2000 Job time : 19 secs.
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Best Local Similarity 90 1%;
Matches 219; Conservative
                                                                                                                 present invention.
Sequence 698 AA;
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Treatment of Inflammatory Disorders
                                                                           Length 242;
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3 5 1805. 1 44 MF floppy disk
                                                                          Scare 1511, DB 2; I
Pred. No. 2.426-98;
18; Mismatches 12;
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STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                   TOPOLOGY: Linear
CE 242 AA; 26430 MW, 332270 CM,
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APPLICANT: Fong, Sherman
APPLICANT: Hebert, Caroline Alice
APPLICANI: Kim, Kyung Jin
APPLICANI: Leong, Steven R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                Sequence 56, Application US/08398612A Patent No. 5686070 GENERAL INFORMATION:
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APPLICATION NOBER:
FILING DATE: 01-Mar-1995
APPLICATION NUMBER: Application NUMBER:
INFORMATION FOR SEG IS NO. 56. SEQUENCE CHARACTERISTICS:
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                                   : 242 amino acids
Amino Acid
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                                                                           Match
Local Similarity 87.68,
es 212, Conservative
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APPLICANT: Fong, Sherman
APPLICANT: Fong, Sherman
APPLICANT: Kim, Kyung Jin
APPLICANT: Kim, Kyung Jin
APPLICANT: Leong, Steven R.
TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment of Inflam
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: 1BM PC compatible
OFEPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATIN (Genentech)
SOFTWARE: PATIN (Genentech)
AFFLIGATION NUMBER: "S/OR/398,613A
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STREET + 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                      NAME: Love, Richard B.
PEGISTPATION NUMBER: 34.659
REFERENCE/DOCKET NUMBER: P0874P1
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242 AA, 26430 MW, 332270 CN;
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                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
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TELEX: 910/371-7168
INFOPMATION FOP SEQ ID NO: 56:
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03-MAP-1994
                 INFORMATION:
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Amino Acid
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Local Similarity 87.6%;
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APPLICANT: Fong, 8
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FILING DATE:
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72-09-392-613A-5£
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HILLS F INVENTION: OF HILLAMMATORY DISORders
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13. júly – 18. september 1910 – 14. martin 1919 – 14. martin 1919 – 18. martin 1919 – 18. september 180
22. hvplifyggterlengalski lettalikastasvvillinge bænzunnu 180
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PPED GW: Librar
FB: 242 AA, 2414 MW, 33220 GM,
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Application 08/08398611A
Patent No. 57.2946
CHERDAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABELITANI Bolod, Shorman
ABELITANI Bolomay, Carolino Alice
ABELITANI Kum, Kyung alic
APELITANI Loona, Steppen K.
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PROFESTIONS MARKET 99,201954
FILLING DATE: 97-MARK-194
ALPENDING WELL 97-MARK-194
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FEBEREN FACTOR NUMBER: 77.136
FELEPHENE: 415,225: 1499
FELEPHENE: 415,225: 1499
FELEPHENE: 415,735: 1499
FELEX. 410,731:7194
INDERNATION FOR SEQ. 11: No. 55:
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CNUMY: USA
           FILLING DATES
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TO US --- 499-611A-56
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121 HVELIFSASIKIFLYSAVAAFIVFIKFYSKELLKSSTASVVCLLANIVIFFEAVGAKVUN 180
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17
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APPLICANT: Henner, Dennis J.
APPLICANT: Bass, Steven
APPLICANT: Bass, Steven
APPLICANT: Greene, Pennal
APPLICANT: Greene, Pennal
APPLICANT: Wells, James A.
APPLICANT: Wells, James A.
IIILE OF INVENTION: ENRICHMENT METHOD FOR VARIANT PROTEINS WITH
TITLE OF INVENTION: ALTERED HINDING PROPERTIES
NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                                                                                                                                                           1 MKKNIAFELLASMEVESIAINAYADIQMIQSPSSISASVGTFVTITTESSQSIVHAIGETY 60
                                                                                                                                                                                                                                                                                                                     Age 98. Sector 1911. TB 1. Legali 242. Local Similarity 87.68. Pred. No. 2.426-98. Local Similarity 87.68. Pred. No. 2.426-98. Lin Previous 12. Librix Lin Previous 12. Librix Lin Lin Librix Lin Lin Librix Lin Lin Lin Lin
E.
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CE 141 AA, 1643 NW 33127 CN:
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ID US-08-462-587A-25
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RESULT 6
IP PCT-US91-09133-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 237;
                                                                                         E: 3.5 inch, 1.44 Mb floppy disk
IBM PC compatible
SYSIEM: PC-DoS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1437; DB 2;
Pred No 5.62e-93;
                                                                                                                                                         FILING DATE: 05/70/403/00/A
FILING DATE: 05/70/403/00/A
CLASSIFICATION: 435
PRIOR PAPLICATION: 435
PRIOR APPLICATION DATE: 06/66/058
FILING DATE: 30-APR-1993
PRIOR APPLICATION DATA: APPLICATION NUMBER: 05/70/133
FRICK APPLICATION NUMBER: 07/743614
FILING DATE: 09-AUG-1991
PRIOR APPLICATION NUMBER: 07/743614
FILING DATE: 14-JUN-1991
PRIOR APPLICATION NUMBER: 07/715300
FILING DATE: 14-JUN-1991
PRIOR APPLICATION DATA: 14-JUN-1991
PRIOR APPLICATION DATA: 14-JUN-1991
                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 03-DEC-1990
ATU, NORY, A:ENT INF: PARTITY.
NAME: SCHWATL, TIMOTHY R.
PEGISTPATION NUMBER: 32171
REFERENCE/DECKET INMERE: P0645P4E2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/22-9881
TELEX: 910/371-7168
INFORMATION FOR SECIED NO: 25:
                                                                                                                                                   US/08/463,587A
                    STREET: 460 Foint San Brunc Blvd
CITY: South San Francisco
STATE: California
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                                                                                                                             (Genentech)
                                                                                                                                                                                                                                                                                                                                                                       07/521667
            Genentech, Inc.
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PRIOF APPLICATION DATA
APPLICATION NUMBER: 07/52
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Amino Acid
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LENGIH: 237 amino acids
                                                                                                               OPERATING SYSTEM: PC-D
SOFTWARE: WinDatin (Ge
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                              COMPUTER READABLE FORM: MEDIUM IYPE: 3.5 incl
CORRESPONDENCE ADDRESS:
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Local Similarity 90 1%:
les 218; Conservative
                                                         USA
                                                                      94080
            ADDRESSEE:
                                                                                                       COMPUTER:
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                                                         COUNTRY:
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58 -- WYQQKPGKAPKLLIYSASFLYSGVPSFFSGSFSGTDFTLTTSSLQFEDFATTTCQQHY 115
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TITLE OF INVENTION. Enrichment Method For Variant Proteins
TITLE OF INVENTION: With Altered Binding Properties
NUMBER OF SEQUENCES: 27

COPPESSONDENCE ADDPESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 85.5%; Score 1437; DB 3; Length 237: Rest Local Similarity 90.1%: Pred. No. 5.62e-93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk computER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWAPE: Patin (Genentech) CUPPENT APPLICATION DATA: APPLICATION NUMBER: PCT/US91/09133 FILTERS DATE: 19911203
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
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                                                                                                                                                                                   Sequence 26, Application PC/TUS9109133 GENERAL INFORMATION
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                                                                                                                                        Sequence 26, Application PC/TUS9109133
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PRIOR APPLICATION NUMBER:
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APPLICATION NUMBER:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
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PESISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: 645
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/266-1489
TELEFAX: 415/952-9881
                                                                                                                                                                                                                          Genentech. Inc.
Garrard, Lisa J.
Henner, Dennis J.
Bass, Steven
Græene, Ronald
Lowman, Henry B.
Wells, James A.
STANDARD
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AMINO ACID
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 ind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  218; Conservative
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AFPLICANT:
APPLICANT:
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APPLICANT:
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194 ALGERMANDEN FROM THE TREE SET IN SKALMERHKVYANDEVIHOUSLESPVIKSENDS 235
181 ALGERMANDEN FROM THE TREE STREET SKALMERHKVYANDEVIHOUSLESPVIKSENDS 240
114 TIPPIPAPIRADIAKUDAKITAAN SVETIREBILJAKSITASVVILLAMEYEKEEAKVIMEVIJA ITE
                                                                        12. HVPC1PTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTSCHIPTS
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APPLICANT: COMMUN. HORRY B.
APPLICANT: LOWERS, Larre A.
APPLICANT: Wells. Larre A.
APPLICANT: Wells. Larre A.
APPLICANT: Wells. Larre A.
APPLICANT: WELLHOWS, LOYID J.
ILLE OF INVENTION: WITH ALTERED SINGING PROPERTIES
WITHER OF CHOCKPRICE F.
WITHER OF CHOCKPRICE F.
WITHERSTONE ROLED BESS:
WITHER OF CHOCKPRICE F.
WITHERSTONE ROLED BESS:
WIT
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"MEDITAL FLORMAN DISK
"WENTER" IRR PO POPEATIBLE
"PERMANEL PATONIN PROCESS."
"PERMANEL PATONIN DATA!

APPETATION NUMBER: 0.05/67/44.667A
FILIN DATE: 0.05.70/14.99.5

APPETATION NUMBER: 0.05/67/44.667A
APPETATION NUMBER: 0.05/67/44.667A
APPETATION NUMBER: 0.05/67/44.667A
APPETATION NUMBER: 0.05/67/44.667A
APPETATION NUMBER: 0.05/67/44.614
BETAIN DATE: 0.05/67/44.614
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Bonnor, Donnie J.,
Bass, Stoven
Sroop, Bonald
Lowman, Honry B.,
Welle, Carrer A.
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Sequence 17, Application 05/08867352B
Patent No. 594511
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard & Prosta, Paulo M. Dardien Tohn Lowe
IIILE OF INVENTION: Improved Paulo Tay Method of
TITLE OF INVENTION: Improving Polypeptides
NUMBERSONEENCE ADDRESS:
                                                                                                                                                                                                                                         121 HVPLIFGGGTKVEIKPTVAABGVPIFPPSPERNIKSGTASVVOLIINNEVPPFAKVLWEVDN 189
                                                                                                                                                                                                                                                                                      116 IIEPIESĮSIKVEIKEIKPIVAAPSVEIFFPSCEĮLKSGIASVVOLLMUFYPPEAKYTWKUM 175
                                                                                                                                                                                            1 MKKNIAFLLASMEVESIATNAVADIQMTQSPSSLSASVGDPVTITTGBALD-VN-TAVA- 55
                                                                                                                                                                                                          F ...
                                                                                                                                              Query Match
Best Local Similarity 90.1%; Pred, No. 5 626-93;
Matches 219, Conservative 5, Mismatches 14, 10.303 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94080
COMPUTER PEADABLE FORM:
MELTIN TYPE: 7 F 1.23., 144 Mt. flight distance to COMPUTER: 1EM PC compatible computer: 1EM PC compatible correct and system for flows, Ms-flow Software: MinPatin (Genetich)
CURRENT APPLICATION DAIA: 05.032/887.3528
FILLIA CALON NOMBER: 05.032/887.3528
FILLIA CALON NOMBER: 05.044
REGISTRATION NOMBER: 05.044
TOPOLOGY: linear
MOLECULE IYPE: protein
JENCE 237 AA, 25977 MM, 322792 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17, Application US/08887352B
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CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genentech, Inc.
                                                                  SEQUENCE CHARACTERISTICS:
LENGTH, 237 arin, avids
TYPE: amino acid
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ADDRESSEE: Gent
Thr. 1 DNA Way
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                                                                                                                                                                                                                                                                                                                                                                               236 EC 237
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                                                                                                                           SECUENCE
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Query Match
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UNMARP OF SEQUENCES: 2
CORPESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                               120 FIFFFSDETLESSIASVVGLLMHYFREAKVQWKVTMALLSJNSTESVTEQDSKFSTYSL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144 FIFPPSDEQLKSGIASVVCLLNNEYFHEAKVQWKVLNALQSGNSGESVIEQUSKCSTYSL 203
                                                                                                                                                                                                                                                                                    5: Mismatches 13; Indels 1: Gaps
                                                                                                                                                                                                                Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER REMARKE FORM:
MEDIUM TYPE: 3 Sinch, 1.44 Mb (Loppy disk COMPUTER: IBM PC compatible.
OPERATING SYSTEM: PC-DuS/MS-DuS SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
AFTLIANTITH NUMBER 15/79/997,3528
FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 80.3%; Score 1350; EE 2; Local Similarity 90 9%; Pred No 1.138-R6; es 199; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPT.
                                                                                                                                                       IOPOLOGY: Linear
SEQUENCE 219 AA; 22800 MW; 271009 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 19, Application US/088873528
Patent No. 5994511
GENERAL INFORMATION:
REFERENCE, DOCKET NUMBER: F1123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650, 225-1489
TELEFAN: 650, 950-9881
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650,525-1489
TELEPAX: 650,952-9881
INFORMATION FOR SEO ID NO: 19:
SEQUENCE CHARACTERISTICS:
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CLIY: South San Francisco
STATE: California
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ATTORNEY/AGENT INFORMATION:
                                                                                                                 LENGIH: 218 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Svoboda, Graig G.
REGISTRATION NUMBER: 39
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                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                    Matches
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APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Jowe TILE OF INVENTION: Improved Anti-1gE Antibodies and Method of TITLE OF INVENTION: Improving Polypeptides NIVER OF SEQUENCES. 26
                                                                                                                                                                                                                                                                                                                                 60 SGVPSRESGSGSGTDFILLISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIKRTVAAFSV 119
                                                                                                                                                                          1 DIQLTQSPSSLSASVGDPVTITCPASKP-VDGEGDSYLNWYQQKPGKAPKLLIXAASYLE 59
                                                                                                                                  Gaps
                                                                                                                                                                                            24 DIQMIQSPSSLSASVGPVTITCPSSQSLVHGIGETYLHWYQYPGKAPKIJIYKVSNPF
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                                                                                          Length 218;
                                                                                        Query Match
Rest Local Similarity 90 9%, Pred No. 1 17e-96,
Matches 199, Conservative 6; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER PEADABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                180 SSTLTLSKADYEKHKVYACEVTHQGLSSFVTKSFNRGEC 218
                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION. 530
ATTORNEY/AGENT INFORMATION:
NAME: SVOPOGA, Craig G.
PROTSTRATION NUMBER: 30.
TELECOMMING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80.3%, Score 1350,
                               TOPOLOGY: Linear
FE 218 AA, 23840 MW: 271009 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 24, Application US/09887352B
Patent No. 5994511
GENERAL INFORMATION:
APPLICANT: HENRY R. Lowman, Leona:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: WinPatin (Genentech)
CUPPENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887.3
FILING DATE: 03-Jul-1997
CLASSIFICATION. 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 24, Application US/08987352B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEFERENCE/DOCKET NUMBER F1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHAPACTEPISTICS:
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-987-352B-24 STANDAPD:
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Amino Acid
218 amino acids
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                Amino Acid
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LENGIH.
                                                      SETTENCE
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Anti-selectin antibodies for prevention of multiple org
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80.3%; Score 1350; DB 3; Longth 218;
Best Local Similarity 90.4%; Pred. No. 1.136-86;
Matches 138; Conservative 6; Mismatches 13; Fobris 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NOT TO THE PROPERTY OF THE PROPERT
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COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Computer Disk

COMPUTER: 1BM PC compatible

OPERATING SYSTEM: pt-ft-S/NS-ft-S

SOFTWARE: ASCII

CUFFERT AFFLICATION DATA:

AFFLICATION NUMBER FOLGS-SOFT-ST-S

FILING DATE:
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ADDRESSEE: Attn: Norman D Hanson
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MOLECULE TYPE: protein
JENCE 218 AA, 23855 MW, 269234 CN:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: U4/578,953
FTITNG DATE: 27-Dec-95
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INFOFMATION FOR SEQ ID NO: 2
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Prof. Lorda Sumilarity 40.9% Prod. No. 1.136-86.
Mirthol. 1991 Castration 50 Mismatches 13; Indels 1: Saps 1:
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A FILTER FOR THE FILTER FOR THE STATE OF THE FILTER FOR FILTER FOR FILTER FOR FILTER FOR FOR FILTER FOR FIL
                                                                                                                                                                                                1 GIULTOROGEISKRUTTUNITITEREN VEGFERSTIMMILIEFFEKELIYARSTEE 59
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MIGHOR TYPE: 1 S 10-01, 1.44 Mb floppy disk
COMPUTER: 1MM PG compatible
VERBALING SYSIEM: PC-CONSTERS:
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CDRRENT APPLICATION DATA:
APPLICATION NOMESE, US, "9, 99", 212R
FILIND DATE: 03-501-1997
CLASSIFICATION: 8-30
ATTHREY/A FET INTERNATION
NAME: SPENDAR CHARLE SPENDAR CHARLESCHAFFN WINREPP. 39,044
POTERNATION WINREPP. 39,044
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TYPE: Acids Acid
14 P.D.Y. Linear
TE 214 AA: 24499 MM: 271094 CN:
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TELLIPHTNES 650,005-1499
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CITY: SOUTH SAN Francisco
SIAIE: California
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APPLICANT: Hebert, Caroline A. APPLICANT: Kabakoff, Phona C APPLICANT: Mosey, Mark W. TILLE OF INVENTION 1: 9 Antagorists [ir Treatment of Inflammatrine of Invention: Disorders and Asthma
                                                                                                                                            144 FIEPPSDEQLKSGIASVVCLLMMFYPPEAKVQWKVDMALGSGNSQESVTEQDSFPSTYS: 203
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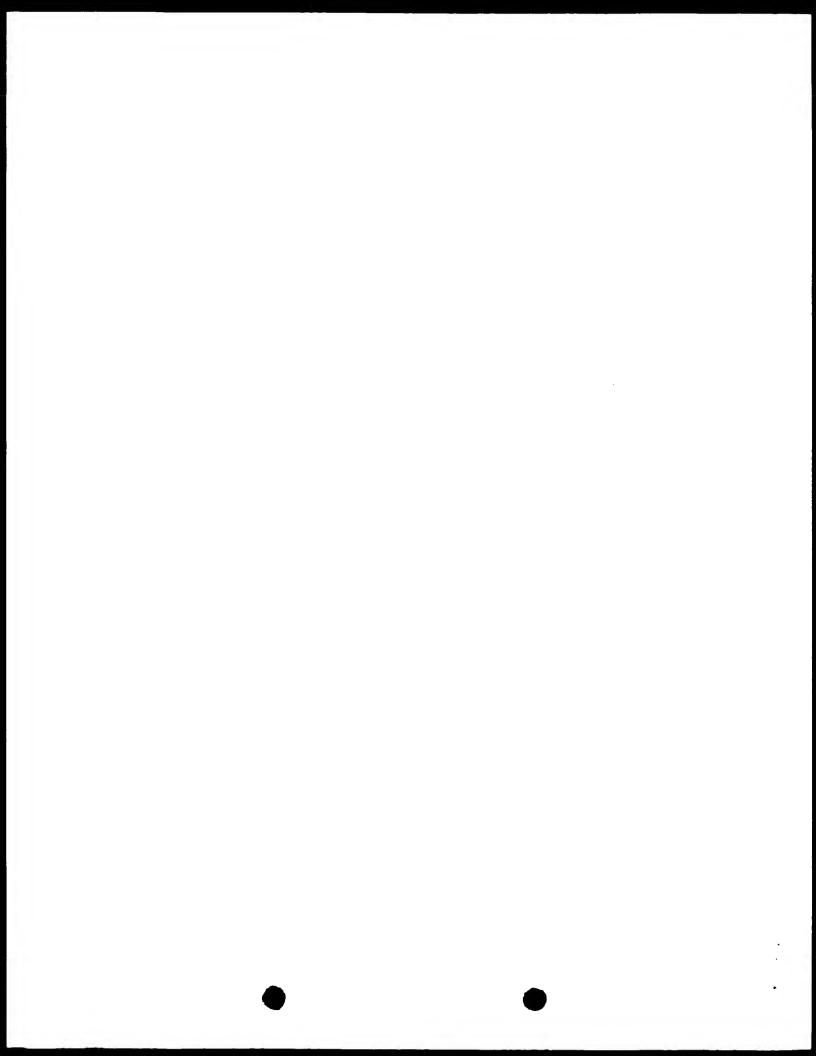
79.7%: Score 1340; DB 2; Length 237:
Best Local Similarity 81.8%: Pred. No. 5.97e-86;
Matches 198; Conservative 19; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                              180 SSTLTLSKADYEKHKVYAGEVTHQGLSSPVTKSFWRGEC 218
                                                                                                                                                                                                                                                                                                             204 SSTLTLSKADYEKHKVYAGEVTHQGLSSPVTKSFNPGET 242
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STYPET' 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
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237 AA: 26087 MW; 317816 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P0874P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 28, Application HS/08491334A Patent No. 5874080 GENEPAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 28. Application US/08491334A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: WinPatin (Genentech) CURRENT AFFLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEFERENCE/POCKET NUMBER: PO
TELECOMMUNIONATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD
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Amino Acid
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INFORMATION FOR SEQ ID NO-
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SECUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
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IIILE OF INVENTION: Improved Anti-IgE Antibodies and Method of
IIILE OF INVENTION: Improving Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                          84 SOVESBESGSGSGILFILLISSLQFERTATYYTSSSTHVPILTFGGGTKVEIKPTVAAFSV 143
                                                                                                                                                                                                                                                                                                                                                 120 FIFFFSSSELESSIASVVSLINNEYPPSAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 SGVPSKESGSGIDFILIISSLAFEDFATYYOQQSHEDFYTFGQGTKVEIKPTVAAPSV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2: PICHTERFER AND THE PROBLEM OF THE PROBLEM OF THE PROBLEM OF BRANCH PROBLEM OF THE PROBLEM OF 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 DIEMILSPSSISASVSEPVITTTPSSESTVHSISETYLHWYQQKPGKAPKILIYKVSNPF 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Mismatches 13; Indels 1; Gaps
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79.8%; Score 1342, DB 2, Length 218; Best Local Similarity, 90 4%; Pred. No. 4 280-86.

Matches 198; Conservative 7; Mismatches 13; Indels
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MEDIUM TIFE: 3.5 Inch, 1.44 Nb flughy disk
COMPUTER: IRM PC COMPUTER:
CERATINS SYSTEM: 90-DOS/MS-FOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 SSILILSKADYEKHKVYACEVIHQGLSSFVIKSFNRGEC 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          204 SSILILSKADYEKHKVYACEVIHQGISSPVTKSFNRGEG 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #525, 7887, 952P
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: 18,709,787,357
ELLING DATE: 03-011-1997
CLASSIFICATION: 530
ATTICKEY, ATENT INTERMATION
NAME: SVODOGA, CRAYG R
REGISTRATION NUMBER: 39,044
EEFERENTE, DOCKET NUMBER: F1123
FELECOMMUNICATION INPORMATION:
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D18 AA, 23900 MW, 271194 CN,
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INFORMATION FOR SEG IN NO. 13.
SEQUENCE CHARACTERISTICS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 650/225-1489
650/952-9881
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Amino Acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T 13
US-08-887 352B-12
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117 DECEMBER OF CONTROL OF CONTROL OF STANDARD TERROR OF STANDARD 
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APPLIANT: Font, Sherman
APPLIANT: Hobert, Caroline Alice
APPLIANT: Hobert, Caroline Alice
APPLIANT: Locar, Stoven R.
THE OF INVENTION: AutilLE-8 Monoclonal Antibodies for
THE OF INVENTION: Inequired, of Inflammatory Disorders
NUMBER OF SECTIONES: 58
PURENEW NUMBER OF SECTIONES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              237 AA.
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MEDISM TYPE: 3.5 inch, 1.44 Mb (loppy disk COMPUTER: 18M PC compatible OPERATINS SYSTEM: PC-DYS/MS-DGS SOFTWARE: WIRBATIN (Generacch)
UDPRENI APPLICATION DATA:
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South San Francisco
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FILINI DATE: 91-MAP-1995
APPLICATION NUMBER: 98/25864
ALLOHRIY PARENT INDEMATION:
NAME: LOVO, BICHART B.
PREHERINITON NUMBER: 44,659
PREHERINITON NUMBER: 46,659
PREHERINITON NUMBER: 76,659
PREHERINITON NUMBER: 76,674
FILEPOMMUNICATION INDEMATION:
TELLEPOMMUNICATION AND APPLICATION:
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TYPE: Action Acid
Telegrat: Linear
NY: Acid 25037 MW: x17916 CN:
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: USA
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Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, E.; Yamaki, S.; Koci, H.; Takashi, I.; Shinoda, T submitted to Jipilo. November 1998
A new subgroup of k type light chains (VkV) identified in cases of AL amyloidosis.
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A new subgroup of k type light chains (VkV) identified in cases of AL amyloidosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94 SGVPSPESGSGSGIDETLIISSLOPEDPATYYGSG-STHVPITFGGGTKVETKPTVAAPS 142
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                                                                                                                                                                                                                                                                                                                                         Gaps
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05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change
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                                                                                                                                                                                                    1-215 ##label ALI
#length 215 #molecular-weight 23463 #checksum 78
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Ig kappa chain V-III (KAU cold agglutinin) · human
                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                  72.8%; Score 1224; DB 2; Length 215; 82.3%; Pred. No. 7.47e-173;
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Ig kappa chain NIG93 precursor - human
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Best Local Similarity 80.5%, Fred. No. 8.37e-166,
Matches 177; Conservative 17, Mismatches 20,
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                                                                                                                                                                                                                                                                                                                                            18; Mismatches 15;
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                                                                                                                                  #authors Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.
#journal J. Biol. Chem. (1991) 266:2836-2842
#title The primary structure of the Fab fragment of protein KAU,
#cross-references MUID:91131575
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M.; Takashi, I.; Shinoda, T.

submitted to JIPID, November 1998
Structure rolationship of kappatype light chains with AL
amyloidosis: Multiple deletions found in a VeTV protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 SGVPSRFSGSGSGIDFILIISSLQPEDFATYYCSQSTHVPLTFGQGTKVEIKRTVAAPSV 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EIVLIQSPAILSLSPGERAILSGGASQS-V-S-SN-YLAWYQQKPGQAPRILIYDASSRA 56
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Ig Kappa chain Ama7 precursor - human
#formal_name Homo sapiens *common_name man
05-Dec-1998 *sequence_revision 05-Dec-1998 *text_change
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#formal_name Homo sapiens #common_name man
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#length 216 #molecular-weight 23926 #checksum 4862
                                                                                                                                                                                                                                                                                                                                                                                            heterotetramer: immunoglobulin
#length 215 #molecular-weight 23050 #checksum 116
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Pred. No. 8.78e-158;
15; Mismatches 32; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 67.8%; Score 1140; DB 2; Length 219
Local Similarity 80.3%: Pred No. 4.31e-159;
Les 175; Conservative 16; Mismatches 23; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    204 SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNPGE 241
                                                                                                                                                                                                                                                                                                                                   ##molecule_type protein
##residues 1-215 ##label LEO
                                                                                                                                                                                                                                                                                                              preliminary
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Best Local Similarity 77.2%;
Matches 169; Conservative
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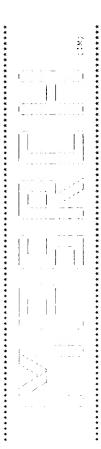
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į.	"The covalen	"The covalent structure of a human gamma G	a human g	gamma G-immunoqulobulin. VI. Amino
E	acid sequence	e of the light	chain.";	
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	Gall W.E., Ec	delman G.M.:		
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Ļ., Ω.,	denes conser	ve homology in	functiona	a] sogmonts.";
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147200; -
Mew York (1969).
[6]
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MEDLINE; 83178921
Novotny J., Margolies M.N.;
"Amino acid sequence of the light chain variable region from a mouse anti-digoxin hybridoma anti-doxin hybridoma anti-doxin hybridoma anti-doxin hybridoma sequence of the Novotna Novot
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---- MISCELLANDOGS: THIS CHAIN WAS ISCLATED FROM A WALDENSTROM'S MACROGLOBULIN.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 1.01e-115;
20: Mismatches 13; Indels
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6 7 CMPLEMENTARITY-DETERMINING
7 7 CMPLEMENTARITY-DETERMINING
8 107 FRAMEWORK 4.
8 108 BY SIMILARITY.
8 AA, 11777 MW, 828324A24125827E CRC64;
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Immusoglobulin V region: Monoclonal antibody: Hybridoma
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12273 MW, F9F39CE949A84C2A GRC64;
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15-JUL-1999 (Rel. 38, Last annotation update)
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ALIGNMENTS

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Score 227, DB 4; Length 397;
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C3: Xismatches 98; Indels 21: Gags 29;
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01-NOV-1998 (IrEMBLrel. 08, Last sequence update)
11-NOV-1998 (TEMBLrel. 12, Last sequence update)
PROTEIN TYROSINE PHOSPHAIASE, NON-PECEPTOR TYPE SUBSTPATE 1 PRECURSOR
SHP SUBSTRATE-1) (INHIRITORY RECEPTOR SHPS-1) (SHPS-1) (SIGNAL-
RECULATORY PROTEIN ALPHA-1) (SIRP-ALPHAI) (MYD-1 ANTIGEN)
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Eutheria, Primates, Catarrhini, Hominidae, Homo.
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01-NOV-1999 (TYEMBLEC) 12, Last sequence update)
01-NOV-1999 (TYEMBLEC) 12, Last annotation update)
DJS76H24 2 (SIRP-BETAI (SIGNAL REGULATORY PROTEIN BETA 1))
HOMO Sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JUN-1999) to the EMBL/G-mBank/PDRJ databases EMBL: AL049634; CAB46661.1; -. SEQUENCE 397 AA 420477 MW; COPA1PCS CPC32;
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Gaps 17;
-:- SUBCELLULAP LOCATION: TYPE I MEMBRANF PROTEIN
-:- TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST LEVELS IN BRAIN.
HIGH LEVELS ALSO PRESENT IN HEART, SPLEEN, TESTIS, OVARY AND PEPIPHEPAL BLOOD LEUKOCYTES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 LT-FGGGTKVEIK-PTVAAPSVFIFPPSPEGLKSGTASVVCLLNNFYPPFFAKVQW-KVDN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72 -AG-FAPELIYNQKEGHFPPVITVSESTMPENNDFSISISMITPADAGTYYCVMFPMGSF 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 KPSKAPKILIYKVSN-RFSGVPSRFSGSGSGT-DFTLTISSIQPEDFATYYGSQ-STHVP 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 FLLASMEVESIAINAYADIQMIQSPSSLSASVGDRVIIICRSSQSLVHGIGETYLHWYQQ 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 EDLAASCAWSGVAGE-EELQVIQPDKSVSVAAGESAILHCIVI-SLIF-VG-F-IQWFRG 71
                                                                                                                                               -:- SIMILARITY: BELONSS TO THE IMMUNOSLOBULIN SUPERFAMITY CONTAINS TWO CLIKE AND ONE V-LIKE DOMAINS.
EMBL: 056043: AAA12974 1. - .
EMBL: Y10375; CAA71403.1; -.
                                                                                                                                                                                                                                                 Signal; Transmembrane; Alternative splicing: Immunoglobulin domain; 31/coprotein; SH3-binding: Phosphorylation.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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IG-LIKE C1-TYPE DOMAIN.
IG-LIKE C1-TYPE DOMAIN.
IG-LIKE C1-TYPE DOMAIN.
SH2-BINDING (POTENTIAL).
SH2-BINDING (POTENTIAL).
SH2-BINDING (POTENTIAL).
SH2-BINDING (POTENTIAL).
PHOSPHOPYLATION (POTENTIAL).
                                                                                                                                                                                                                                                                                            PPOTEIN TYPOSINE PHOSPHATASE,
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Best Local Similarity 25,5%: Pred. No. 2 256-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 ALOSGNSQESVIEGDSKDSTYSLSSTLILSKADYEKHKVYACEVTHOGL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHOSPHORYLATION (POTENTIAL). PHOSPHORYLATION (POTENTIAL).
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01-NOV-1998 (ITEMBLIEL 08, Last sequence update)
01-NOV-1998 (ITEMBLIEL 11, Last annotation update)
01-AUG-1999 (ITEMBLIEL 11, Last annotation update)
SIGNAL-PEGULAIORY PROTEIN BEIA-1 PPECIFSOP (SIRP-BEIAL).
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